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OM protein - protein search, using sw model

Run on: June 21, 2004, 10:18:09 ; Search time 65.5868 Seconds
(without alignments)
4734.482 Million cell updates/sec

Title: US-10-658-782-6
Perfect score: 5912
Sequence: 1 MATRAVCVLKGGPVGQIIN.....GNKDRRSTGKSGKPGYWP 1099

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	5912	100.0	1099	5	AAU76378	Aau76378 HCV multi
2	5912	100.0	1099	6	ABG72262	Abg72262 HCV multi
3	4032	68.2	829	5	AAE18690	Aae18690 Multiple
4	4032	68.2	829	7	ADC06769	Adc06769 Chimeric
5	3829.5	64.8	1021	2	AAW34481	Aaw34481 HCV anti
6	3829.5	64.8	1021	2	AAW40039	Aaw40039 Fusion pr
7	3829.5	64.8	1021	5	AAE22050	Aae22050 pSOD/c200
8	3050.5	51.6	841	2	AAE68547	Aae68547 HCV prote
9	3050.5	51.6	841	6	ABO27020	Abo27020 Hepatitis
10	3050.5	51.6	841	7	ADA07875	Ada07875 HCV prote
11	3047.5	51.5	841	2	AAW01701	Aaw01701 hSOD-HCV
12	3047.5	51.5	841	2	AAW46397	Aaw46397 Amino aci
13	3047.5	51.5	841	2	AAW97609	Aaw97609 Amino aci
14	3042.5	51.5	840	2	AAE14349	Aae14349 HCV prote
15	2909.5	49.2	2261	1	AAE90164	Aap90164 Peptide e
16	2909.5	49.2	2436	1	AAE92050	Aap92050 Sequence
17	2909.5	49.2	2436	1	AAE90288	Aap90288 Peptide e
18	2909.5	49.2	2772	3	AAE18540	Aab18540 Protein e
19	2909.5	49.2	2955	2	AAE14975	Aay14975 Amino aci
20	2909.5	49.2	2955	3	AAE18541	Aab18541 Polypepte
21	2909.5	49.2	3011	2	AAE90931	Aar90931 Hepatitis
22	2909.5	49.2	3011	2	AAW34480	Aaw34480 HCV polyp
23	2909.5	49.2	3011	2	AAW40038	Aaw40038 HCV polyp
24	2909.5	49.2	3011	5	AAE22049	Aae22049 Hepatitis
25	2906.5	49.2	2301	1	AAE92047	Aap92047 Sequence

ALIGNMENTS

RESULT 1

AAU76378
ID AAU76378 standard; protein; 1099 AA.

XX AAU76378;

XX 08-MAY-2002 (first entry)

DT HCV multiple epitope fusion antigen (MEFA) 7.1 protein sequence.

DE Hepatitis C virus; HCV; NS3/4a conformational epitope; seroconversion;
KW Immunoassay solid support; multiple epitope fusion antigen; MEFA;
KW non-structural protein.

XX Hepatitis C virus.

OS Synthetic.

XX WO200196870-A2.

XX 20-DEC-2001.

XX 14-JUN-2001; 2001WO-US019156.

XX 15-JUN-2000; 2000US-0212082P.

XX 02-APR-2001; 2001US-0280811P.

XX 02-APR-2001; 2001US-0280867P.

XX (CHIR) CHIRON CORP.

XX Chien DY, Arcangel P, Tandeske L, George-Nascimento C, Coit D;

XX Medina-Selby A;

XX WPI; 2002-090228/12.

XX N-PSDE; ABK15345.

XX Immunoassay solid support, useful for detecting hepatitis C virus
infection in biological sample, comprises HCV NS3/4a conformational
epitope and multiple epitope fusion antigen bound to the support.

XX Claim 5; Fig 5; 92pp; English.

XX The present invention relates to a new immunoassay solid support
consisting essentially of at least one hepatitis C virus (HCV) NS3/4a
conformational epitope and a multiple epitope fusion antigen (MEFA),
bound to the support. The NS3/4a conformational epitope and/or MEFA
reacts specifically with anti-HCV antibodies present in a biological
sample from an HCV-infected individual. The immunoassay of the invention
is useful for detecting hepatitis C virus infection in a biological

sample. The method of the invention provides a sensitive, accurate diagnostic and prognostic tool to provide adequate patient care and to prevent transmission of HCV by blood and by blood products, or by personal contact. Use of NS3/4a conformational epitope in combination with MEFA, provides a sensitive and reliable method for detecting early HCV seroconversion. Use of MEFA has the added advantages of decreasing masking problems, improving sensitivity in detecting antibodies by allowing a greater number of epitopes on a unit surface area of substrate, and improving substrate. Detection accuracy is increased and the incidence of false results is reduced because of the identification and the use of highly immunogenic HCV antigens which are present during the early stages of HCV seroconversion. The present amino acid sequence represents the multiple epitope fusion antigen (MEFA) 7.1 of the invention

XX Sequence 1099 AA;

Query Match 100.0%; Score 5912; DB 5; Length 1099;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1099; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATKAVCVLKGDPVQGIINFEQKESNGPVKVGSIKGLTEGLHGHVHEFGDNTAGCTS 60
 Db |||

QY 61 AGPHNPISRKHGPKDBERHVDLGNVTADKGVADVSIEDSVISLSGDHCHIIIGRTLVV 120
 Db |||

QY 121 HEKADLKGNEESTKTGNAGSLACGVIGTAQNLNSCNCISYIPGHITGHRMAWKLGS 180
 Db |||

QY 181 AARTTSFVSLFAPGAKQNEHTVTCGAARTTSGLTSLFSPCASQNIQLIVDFIPEVNE 240
 Db |||

QY 241 TTMSRPFVTDNSPPVPSQVQVLAHPTSGKSTKVPAAVAAQYKVLNPSVAATL 300
 Db |||

QY 301 GFAYMSKAHGDINIRTVGRTITGSPITVSTYTKFLADGCGSGAGVDIIICDECHSTD 360
 Db |||

QY 361 ATSLIGTGLDQAEATAGARLVLAATATPPGCVTPHPIREVALSTTGBIPFYGKATPL 420
 Db |||

QY 421 EVIKGGHLLFCHSKKCKDELAALKVALGINAVAYRGLDVSIVPTSGDVVVVATDALMT 480
 Db |||

QY 481 GYTGFDSVLDNCTCVTQVDFSDPTFTIITLPQDAVSRTOBRTGKGIYRFV 540
 Db |||

QY 541 APERSPGMFDSVLCYCYDAGCAWYELTPAETTVLRAYNTPLPVCQDHLFWGCVF 600
 Db |||

QY 601 TGLTHIDAHFLSQTQSGENLPYLVAQVATVCARAQAPPSPDQMWKCLIRLKPTRLHPT 660
 Db |||

QY 661 PLLYRLGAVQNEITLHPVTKYIMTCSADLEVVTSSACSGKPAIIPREVLYRFEDEEE 720
 Db |||

QY 721 CSQHLPIEQQMMLAEQFKALGLSRGKGPALIVPDKVLYQQYDEMECSQAAPYIEQA 780
 Db |||

QY 781 QVIAHQKKEKVLGLIDNDQVVTDPKEILYEAFDEMEECASKAALIEEGORMAEMLSKI 840
 Db |||

QY 841 QGLLGLIRRHVGPGEAGAVQWNRLLIAFASRGNNHVSPTHVPSRSRRPFAQALPVWARPDPY 900
 Db |||

QY 901 PELVETWKKPDYEPVHVHGRSRRFAQALPVWARPDPYPLVETWKKPDYEPVHVHGRKT 960
 Db |||

QY 961 KENTNRPPQDVKPPGGGQIVGRGGPIPKARPEGRTPAQPGYPWPPLYGNKDRRSTGKSW 1020
 Db |||

QY 1021 GKPGYPWPPEKTKRNTNRPPQDVKPPGGGQIVGRGGPIPKARPEGRTPAQPGYPWPPLYG 1080
 Db |||

QY 1081 NKDRRSTGKSWGKPGYPWP 1099
 Db |||

RESULT 2
 ABG72262
 ID ABG72262 standard; protein; 1099 AA.
 AC ABG72262;
 XX
 DT 06-MAR-2003 (first entry)
 DE HCV multiple epitope fusion antigen 7.1 (MEFA 7.1).
 KW Immunoassay solid support; Hepatitis C Virus type-1; HCV-1; HCV-2;
 MEFA 7.1; anti-HCV antibody; NS3/4a conformational antigen; HCV-3;
 HCV infection; Hepatitis C Virus type-2; Hepatitis C Virus type-3;
 mutant; mucin.
 XX Hepatitis C virus type 1.
 OS Hepatitis C virus type 2.
 OS Hepatitis C virus type 3.
 OS Synthetic.
 OS Chimeric.
 XX
 FH Key
 FT Region 1. .156
 FT /note= "Correspond to amino acids 1-156 of HCV-1 hSOD
 superoxide dismutase)"
 FT 159. .176
 FT /note= "Correspond to amino acids 303-320 of HCV-1 E1"
 FT 179. .199
 FT /note= "Correspond to consensus sequence of amino acids
 390-410 of HCV-1 E2 HVR"
 FT 200. .230
 FT /note= "Correspond to consensus sequence of amino acids
 384-414 of HCV-1 and HCV-2 E2 HVR"
 FT 231. .696
 FT /note= "Correspond to amino acids 1193-1658 of HCV-1
 helicase"
 FT 699. .745
 FT /note= "Correspond to amino acids 1689-1735 of HCV-1 5-1-
 1 epitope"
 FT 748. .794
 FT /note= "Correspond to amino acids 1689-1735 of HCV-3 5-1-
 1 epitope"
 FT 797. .843
 FT /note= "Correspond to amino acids 1689-1735 of HCV-2 5-1-
 1 epitope"
 FT 846. .881
 FT /note= "Correspond to amino acids 1901-1936 of HCV-1

FT Region polypeptide C100"
FT 884..919
FT /note= "Correspond to amino acids 2278-2313 of HCV-1 NS5
FT region"
FT 922..957
FT /note= "Correspond to amino acids 2278-2313 of HCV-1 NS5
FT region"
FT 958..1028
FT /note= "Correspond to core region antigenic determinants
FT from amino acids 9-32, 39-42 and 64-88 of HCV-1 and amino
FT acids 67-84 of HCV-2"
FT 1029..1099
FT /note= "Correspond to core region antigenic determinants
FT from amino acids 9-32, 39-42 and 64-88 of HCV-1 and amino
FT acids 67-84 of HCV-2"
XX US2002146685-A1.
XX
XX 10-OCT-2002.
XX
XX 14-JUN-2001; 2001US-00881654.
XX
XX 15-JUN-2000; 2000US-0212082P.
PR 02-APR-2001; 2001US-0280811P.
PR 02-APR-2001; 2001US-0280867P.
XX
XX (CHIE/) CHIEN D Y.
PA (ARCA/) ARCANGEL P.
PA (TAND/) TANDESKE L.
PA (GEOR/) GEORGE-NASCIMENTO C.
PA (COIT/) COIT D.
PA (MEDI/) MEDINA-SELBY A.
XX
XX Chien DY, Arcangel P, Tandeske L, George-Nascimento C, Coit D;
PI Medina-Selby A;
PI
XX WPI; 2003-147573/14.
DR N-PSDB; ABX14411.
XX
XX Immunoassay solid support for detecting Hepatitis C Virus infection in
PT biological samples, comprises Hepatitis C Virus conformational epitope
PT and multiple epitope fusion antigen.
XX
XX Claim 25; Fig 5A-5F; 45pp; English.
XX
XX The present invention relates to immunoassays comprising Hepatitis C
CC Virus (HCV) NS3/4a conformational epitope and multiple epitope fusion
CC antigen (MEFA), bound to a solid support. The NS3/4a epitope and/or the
CC multiple epitope fusion antigen react with anti-HCV antibodies present in
CC a biological sample from an HCV-infected individual. The immunoassays and
CC methods of the invention are useful for detecting HCV infection in a
CC biological sample. The inventive immunoassay solid support provides a
CC sensitive and reliable method for detecting early HCV seroconversion. The
CC assays can detect HCV infection caused by any six known genotypes of HCV.
CC The use of the multiple epitope fusion proteins decreases masking
CC problems, improves sensitivity in detecting antibodies by allowing a
CC greater number of epitopes on a unit area of substrate, and improves
CC selectivity. The present sequence represents HCV multiple epitope fusion
CC antigen 7.1 (MEFA 7.1), a mutant HCV polypeptide derived from various
CC regions of HCV type 1, 2, or 3 (HCV-1, HCV-2, or HCV-3) polypeptide
CC sequences
XX
XX Sequence 1099 AA;
SQ
Query Match 100.0%; Score 5912; DB 6; Length 1099;
Best Local Similarity 100.0%; Pred No. 0;
Matches 1099; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATKAVCVLKGDFVQGIINFEQKESNGPVKVGSIKGLTEGLHGFHVEFGDNTAGCTS 60
DB 1 MATKAVCVLKGDFVQGIINFEQKESNGPVKVGSIKGLTEGLHGFHVEFGDNTAGCTS 60
QY 61 AGPHFNPLSRKHGGPKDEERHVGDLGNVTADKDGADVSDSVISLSDGHCIIIGTLV 120

DB 61 AGPHFNPLSRKHGGPKDEERHVGDLGNVTADKDGADVSDSVISLSDGHCIIIGTLV 120
QY 121 HEKADDLGKGGNEESTKTGNAGSRLACGVIGIAQNLSNCNCISYIPGHITGHRMAWKLS 180
DB 121 HEKADDLGKGGNEESTKTGNAGSRLACGVIGIAQNLSNCNCISYIPGHITGHRMAWKLS 180
QY 181 AARTSGFVSLPAPAKONETHVTGAAARTTSGLTSLFSPGASQNIQLIVFIPVENLE 240
DB 181 AARTSGFVSLPAPAKONETHVTGAAARTTSGLTSLFSPGASQNIQLIVFIPVENLE 240
QY 241 TTMRSFVFTDNSPPVVPQSFQVAHLHAPTGSCKSTKPAAYAAQYKVLVLPNSVAATL 300
DB 241 TTMRSFVFTDNSPPVVPQSFQVAHLHAPTGSCKSTKPAAYAAQYKVLVLPNSVAATL 300
QY 301 GFAYMSKAHGDIPNIRTVRTITTSPTTYTGYKFLADGGCSGGAYDIIICDECHSTD 360
DB 301 GFAYMSKAHGDIPNIRTVRTITTSPTTYTGYKFLADGGCSGGAYDIIICDECHSTD 360
QY 361 ATSLIGIGTVLDQAETAGARLVVLATATPPGTVTPHPNIEVALSTTGEIPYGAIPL 420
DB 361 ATSLIGIGTVLDQAETAGARLVVLATATPPGTVTPHPNIEVALSTTGEIPYGAIPL 420
QY 421 EVIKGGRHLIFCHSKKKCDLAAKLVALGINAVAYYRGLDVSVIPTSGDVVVATDALMT 480
DB 421 EVIKGGRHLIFCHSKKKCDLAAKLVALGINAVAYYRGLDVSVIPTSGDVVVATDALMT 480
QY 481 GYTGFDSVIDCNTCVTQTVDFSLDPTFTIETITLFPQDAVSRTRGRGKPGIYRFV 540
DB 481 GYTGFDSVIDCNTCVTQTVDFSLDPTFTIETITLFPQDAVSRTRGRGKPGIYRFV 540
QY 541 APGERPSGMFSDSVLCECYDAGCANYELTPAETTVLRLAYMNTTGLPVQDHLFEGEVF 600
DB 541 APGERPSGMFSDSVLCECYDAGCANYELTPAETTVLRLAYMNTTGLPVQDHLFEGEVF 600
QY 601 TGLTHIDAHFLSQTQKSGENLPLVAVQATVCARQAAPPSPDWDMKCLIRLKTLLHGT 660
DB 601 TGLTHIDAHFLSQTQKSGENLPLVAVQATVCARQAAPPSPDWDMKCLIRLKTLLHGT 660
QY 661 PLLYRLGAVQNEITLTHPVTXIMTCSADLEVVTSACSGKPAIIPDREVLYREFDEME 720
DB 661 PLLYRLGAVQNEITLTHPVTXIMTCSADLEVVTSACSGKPAIIPDREVLYREFDEME 720
QY 721 CSQHLPYIEQGMMLABQFKQKALGLSRGKPAIVDPKVLVYQYDMEECQAAPYIEQA 780
DB 721 CSQHLPYIEQGMMLABQFKQKALGLSRGKPAIVDPKVLVYQYDMEECQAAPYIEQA 780
QY 781 QVTAHQFKEKVLGLINDQVVTDPKEILYEAPEDEMEECASKAALIEEGORMAEMLSKI 840
DB 781 QVTAHQFKEKVLGLINDQVVTDPKEILYEAPEDEMEECASKAALIEEGORMAEMLSKI 840
QY 841 QGLLGLIRRHVGFEGEGAVQMMNRLIAFASRGNHVSPTHYVPSRSRFAQALPVWARPYN 900
DB 841 QGLLGLIRRHVGFEGEGAVQMMNRLIAFASRGNHVSPTHYVPSRSRFAQALPVWARPYN 900
QY 901 PLLVETWKPDYEPVPHVHGRSRRFAQALPVWARPYNPLVETWKPKDYEPVPHVGRKT 960
DB 901 PLLVETWKPDYEPVPHVHGRSRRFAQALPVWARPYNPLVETWKPKDYEPVPHVGRKT 960
QY 961 KRNTNRRPDVFPFGGGQIVGRRGPPIPKARPEGRRTWAQPGYPWLYGNKDRRSTGKSW 1020
DB 961 KRNTNRRPDVFPFGGGQIVGRRGPPIPKARPEGRRTWAQPGYPWLYGNKDRRSTGKSW 1020
QY 1021 GKPEGFWPRKTKRNTNRRPDVFPFGGGQIVGRRGPPIPKARPEGRRTWAQPGYPWLYGN 1080
DB 1021 GKPEGFWPRKTKRNTNRRPDVFPFGGGQIVGRRGPPIPKARPEGRRTWAQPGYPWLYGN 1080
QY 1081 NKDRRSTGKSWKPGYPWP 1099
DB 1081 NKDRRSTGKSWKPGYPWP 1099

RESULT 3

AAW40039
 ID AAW40039 standard; protein; 1021 AA.
 AC AAW40039;
 XX
 DT 26-MAY-1998 (first entry)
 XX
 DE Fusion protein c200/c22.
 XX
 KW Hepatitis C virus C domain; HCV; immunological activity; c200/c22;
 XX NS3 domain; NS4 domain; S domain; NS5 domain; fusion protein.
 XX
 OS Synthetic.
 OS Hepatitis virus.
 XX
 PN US5712087-A.
 XX
 XX 27-JAN-1998.
 XX
 XX 12-MAY-1995; 95US-00440519.
 XX
 XX 04-APR-1990; 90US-00504352.
 PR 07-JUL-1992; 92US-00910760.
 XX
 XX (CHIR) CHIRON CORP.
 PA
 XX Kuo G, Houghton M, Choo Q;
 PI
 XX WPI; 1998-119973/11.
 DR N-PDDB; AAV09990.
 XX
 XX Immunoassays for hepatitis C virus antibodies - using combinations of
 PT antigenic fragments of HCV polyprotein.
 XX
 XX Example 6; Fig 4; 59pp; English.
 XX
 XX This sequence represents a fusion protein constructed from the hepatitis
 CC C virus core domain (which is situated at the carboxy terminus of the
 CC fusion protein) and a c200 construct (a fusion of the NS3 and NS3
 CC domains). This protein used in the construction of novel combinations of
 CC HCV antigens that have a broader range of immunological activity than any
 CC single HCV antigen. An example of such an antigen given in this
 CC specification comprises a first antigen containing at least 8 amino acids
 CC of the C domain of the HCV polyprotein and a second antigen comprising at
 CC least 8 amino acids of the NS3 domain, the NS4 domain, the S domain or
 CC the NS5 domain of the HCV polyprotein in the form of a fusion protein, a
 CC physical mixture or bound to a solid matrix
 XX
 XX Sequence 1021 AA;
 SQ
 Query Match 64.8%; Score 3829.5; DB 2; Length 1021;
 Best Local Similarity 67.2%; Pred. No. 5.2e-261;
 Matches 784; Conservative 24; Mismatches 79; Indels 279; Gaps 17;
 QY 1 MATKAVCLKGDGPGVQGLINFEQKESNGPVKWSIKGLTEGLHGHVHFEFGDNTAGCTS 60
 DB 1 MATKAVCLKGDGPGVQGLINFEQKESNGPVKWSIKGLTEGLHGHVHFEFGDNTAGCTS 60
 QY 61 AGPHFPLSKHGKGGPKDDEERHVGDLGNVTADKGVDVSTEDSVISLGDHCHIGRTLVV 120
 DB 61 AGPHFPLSKHGKGGPKDDEERHVGDLGNVTADKGVDVSTEDSVISLGDHCHIGRTLVV 120
 QY 121 HEKADDLGKGGNEESTKTGNAGSLRACGVIGIAQNLSNGCNCISYIPGHITGHRMAWKLS 180
 DB 121 HEKADDLGKGGNEESTKTGNAGSLRACGVIGIAQNLEFGA----- 160
 QY 181 AARTSGFVSLFAPGAKQNETHTVTGGAARTTSLTSLFSPGASQNIQLIVDPIVENLE 240
 DB 161 -----VDFIPVENLE 170
 QY 241 TTRSRPVFTDSSPPVVPQSFQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVLPNSVAATL 300
 DB 171 TTRSRPVFTDSSPPVVPQSFQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVLPNSVAATL 230

QY 301 GFGAYMSKAHGIDPNIRTVGRTITITGSPITTYSTYCKFLADGCGSGAYDIIICDCHSTD 360
 DB 231 GFGAYMSKAHGIDPNIRTVGRTITITGSPITTYSTYCKFLADGCGSGAYDIIICDCHSTD 290
 QY 361 ATSLIGIGTGLDQAEATAGARLVVLATATPPGSVTVPHNIEVALSTTGEIPFYKAIPL 420
 DB 291 ATSLIGIGTGLDQAEATAGARLVVLATATPPGSVTVPHNIEVALSTTGEIPFYKAIPL 350
 QY 421 EVIKGRHLIFCHSKKCKDELAALVALGINAVAYRGLDVSIVPTSGDVVVVATDALMT 480
 DB 351 EVIKGRHLIFCHSKKCKDELAALVALGINAVAYRGLDVSIVPTSGDVVVVATDALMT 410
 QY 481 GYTGFDSVIDCNTCTQTVDPSLPTTETITIPQDAVSTORRGTRGKGGIYRV 540
 DB 411 GYTGFDSVIDCNTCTQTVDPSLPTTETITIPQDAVSTORRGTRGKGGIYRV 470
 QY 541 APGERPSGMFDSVLCBCYDAGCANVELTPAETTVRLRAYMNTPLPVCQDHLFEWGVF 600
 DB 471 APGERPSGMFDSVLCBCYDAGCANVELTPAETTVRLRAYMNTPLPVCQDHLFEWGVF 530
 QY 601 TGLTHIDAHFLSQTQSGENLPYLVAQATVCARQAQPPSWDQWKCLIRLKPILHGT 660
 DB 531 TGLTHIDAHFLSQTQSGENLPYLVAQATVCARQAQPPSWDQWKCLIRLKPILHGT 590
 QY 661 PLYRLGAVONEITLTHPVTKYIMTMSADIEVWTS----- 696
 DB 591 PLYRLGAVONEITLTHPVTKYIMTMSADIEVWTS----- 650
 QY 697 ----ACSGKPAIIPDREVLRYREFDEMECSQHLPYIEQGMMLAEOFKOKALGI-----SRG 748
 DB 651 VORVULSGPAIIPDREVLRYREFDEMECSQHLPYIEQGMMLAEOFKOKALGI-----SRG 710
 QY 749 GKPAIVDPKDEVLYQQYD-----EMEECSQAAPYIEQAQVIAHQFKVKVGLIDNDQVWVT 803
 DB 711 AE-VIAPAVQTNWQKLETFWAKHWNFISGIQYLAGLSTLPG--NPALIASLMAFTAATVS 767
 QY 804 P--DKELIYE-----AFDEMECSKAALIEECQORMAEMLKSKIQL 843
 DB 768 PLTTSQTLLENILGGWVAQAAPGAATAFVGLAGLAGAAIGSVGLGKVLIDILAGYAGV 827
 QY 844 LG-----ILRRHVGPGEAGVOMNRL 864
 DB 828 AGALVAFKINSGEVSTEDLVNLLPAILSPGALVGVVCAAILRRHVGPGEAGVOMNRL 887
 QY 865 IAFASRGHVSPTHYVPSRSRRFAQALPYWARPDYNNPLVETWKKPDYBPVPHVHSSRR 924
 DB 888 IAFASRGHVS-----GNSST- 904
 QY 925 FAQALPVWARPDYNNPLVETWKKPDYEPVPHVHGRKTRNTNRPQDVKPPGGQIVG--- 981
 DB 905 -----NP-----KPKQ-----KKNKRNTRRPQDVKPPGGQIVGVV 936
 QY 982 ---RRGP-----PIPKARPEGRRTWAQPGYFWPLYGK----- 1011
 DB 937 LUPRRGPRGLGVTRATKTSRSQPRGRQPIPKARPEGRRTWAQPGYFWPLYGKGGWAG 996
 QY 1012 ---DRESTGKSGKGPYWPWRKTRN 1034
 DB 997 WLLSPGRSPSWGPTD---PRRRSRN 1019
 RESULT 7
 AAE22050
 ID AAE22050 standard; protein; 1021 AA.
 AC AAE22050;
 XX
 DT 16-JUL-2002 (first entry)
 XX
 DE pSOD/c200/core expression plasmid protein.
 XX
 XX Hepatitis C virus; HCV; antigen; C domain; polyprotein; NS3 domain;

NS4 domain; S domain; NS5 domain; pSOD/c200/core plasmid.

KW NS4 domain; S domain; NS5 domain; pSOD/c200/core plasmid.
 XX Hepatitis C virus.
 OS Unidentified.
 OS Chimeric.

Key Location/Qualifiers
 Region 1..154
 /note= "hsod"
 Region 155..159
 /note= "Linker region"
 Region 160..899
 /note= "HCV c200"
 Region 900..902
 /note= "Linker region"
 Region 903..1021
 /note= "HCV c22"

US6312889-B1.

06-NOV-2001.

12-MAY-1995; 95US-00440549.

04-APR-1990; 90US-00504352.

07-JUL-1992; 92US-00910760.

(CHIR) CHIRON CORP.

Houghton M, Choo Q, Kuo G;

WPI; 2002-040268/05.

N-ESDB; AAD35044.

Combination of hepatitis C viral (HCV) antigens, useful in improved immunoassay for detecting HCV antibodies.

Example 6; Fig 4; 58pp; English.

The invention relates to combination of hepatitis C viral (HCV) antigens that have a broader range of immunological reactivity than any single HCV antigen. The combinations consist of an antigen from the C domain of the HCV polypeptide, and at least one additional HCV antigen from either the NS3 domain, the NS4 domain, the S domain, or the NS5 domain and are in the form of fusion protein, a simple physical mixture, or the individual antigens commonly bound to a solid matrix. The combinations of antigens provides broad range immunoassays for anti-HCV antibodies. The invention therefore provides a method for detecting antibodies to HCV in a mammal suspected of containing such antibodies. The present sequence is a protein encoded by pSOD/c200/core expression plasmid DNA containing HCV coding sequence

Sequence 1021 AA;

Query Match 64.8%; Score 3829.5; DB 5; Length 1021;
 Best Local Similarity 67.2%; Pred. No. 5.2e-261;
 Matches 784; Conservative 24; Mismatches 79; Indels 279; Gaps 17;

QY 1 MATKAVCVLKGDPVQGIINFEQKESNGPVKVGSIKGLTEGLGHGFHVEFGDNTAGTS 60
 DB 1 MATKAVCVLKGDPVQGIINFEQKESNGPVKVGSIKGLTEGLGHGFHVEFGDNTAGTS 60
 QY 61 AGPHNPLSRKHGPKDDEHVGDLGNVTADKGVADVSIEDSVISLGDHCIIIGRTLV 120
 DB 61 AGPHNPLSRKHGPKDDEHVGDLGNVTADKGVADVSIEDSVISLGDHCIIIGRTLV 120
 QY 121 HEKADDLGKGNESSTKTGNAGSLACGVIGIAQNLNSGCNSIYPGHITGHRVANKLGS 180
 DB 121 HEKADDLGKGNESSTKTGNAGSLACGVIGIAQNLNSGCNSIYPGHITGHRVANKLGS 180
 QY 181 AARTTSFVSLFAPAKQKETHVTGGAARTTSLTSLFSPGASQNIQLIYDFIPVENLE 240
 DB 161 -----VDIFIPVENLE 170

QY 241 TTMRSPVFTDNSSPPVPFQSOVAHLHAPTSGSKTKVPAAVAAOQYKVLNPSVAATL 300
 DB 171 TTMRSPVFTDNSSPPVPFQSOVAHLHAPTSGSKTKVPAAVAAOQYKVLNPSVAATL 230
 QY 301 GFAYMSKAHGIDPNIRGTGRTITTTGSPITTYSTYKFLADGGCGSGAGYDIIICDCHSTD 360
 DB 231 GFAYMSKAHGIDPNIRGTGRTITTTGSPITTYSTYKFLADGGCGSGAGYDIIICDCHSTD 290
 QY 361 ATSLIGIGTVDLDOAETAGARLVWLATATPPGQSVTPHPNIEEVALSTTGEIPFYKAIPL 420
 DB 291 ATSLIGIGTVDLDOAETAGARLVWLATATPPGQSVTPHPNIEEVALSTTGEIPFYKAIPL 350
 QY 421 EVIKGGRHLIFCHSKKCKDELAALKVALGINAVAYRGLDVSVIPSGDVVVVATDALMT 480
 DB 351 EVIKGGRHLIFCHSKKCKDELAALKVALGINAVAYRGLDVSVIPSGDVVVVATDALMT 410
 QY 481 CYTGDFSDVIDCNTCVTQVDFSLDPTFTTITLPODAVSRQRRGTGRGKPGIYRFV 540
 DB 411 CYTGDFSDVIDCNTCVTQVDFSLDPTFTTITLPODAVSRQRRGTGRGKPGIYRFV 470
 QY 541 APGERPSGMFDSVLCYDAGCAYELTPAETTVLRLAYMNTPGLPYCODHLEFEGVVF 600
 DB 471 APGERPSGMFDSVLCYDAGCAYELTPAETTVLRLAYMNTPGLPYCODHLEFEGVVF 530
 QY 601 TGLTHIDAHFLSQTQKSGENLPYLVAOATVCARAQAPPPSWDQWVKCLIRLKPFLHPT 660
 DB 531 TGLTHIDAHFLSQTQKSGENLPYLVAOATVCARAQAPPPSWDQWVKCLIRLKPFLHPT 590
 QY 661 PLYRLGAVQNEITLTHPVTKYIMTMSADLEVVTIS----- 696
 DB 591 PLYRLGAVQNEITLTHPVTKYIMTMSADLEVVTIS----- 650
 QY 697 ---ACSGKPAIIPDREVLVREFDEMECSOHLPIEQGMWLAQFKOKAIGL-----SRG 748
 DB 651 VGRVLSGKPAIIPDREVLVREFDEMECSOHLPIEQGMWLAQFKOKAIGL----- 710
 QY 749 GKPAIVDPKQVLYQOYD-----EMEECSQAAPYTHQAVIAHQFKEKVLGIDNDQVVVT 803
 DB 711 AE-VIAPAVQTNWQKLETFWAKHWNFLSGIYLAGLSTLPG--NPATASLMAFTAATVS 767
 QY 804 P---DKEILYB-----AFDEMEHCASKAALIIEGQMAEMLKSKI OGL 843
 DB 768 PLTTSTQTLLENILGWVAAQALAAPCAATAFVAGIAGAAIGSVGLKVLIDILAGYAGV 827
 QY 844 LG-----ILRRHYGPGGCAVQWNNRL 864
 DB 828 AGALVAFKIMSGEVFPSTEDLVNLLPALSLPGALVGVVCAAILRRHYGPGGCAVQWNNRL 887
 QY 865 IAFASRGNHVSPTHYVPSRRRFAQALPVWARPDPNPLVETWKKPDYEPVWVHGRSRR 924
 DB 888 IAFASRGNHVSPT-----GNSST- 904
 QY 925 FAQALPVWARPDPNPLVETWKKPDYEPVWVHGRKRTNRRPDQVFKPGGQIVG--- 981
 DB 905 -----NP-----KPK-----KKNKNTNRRPDQVFKPGGQIVG 936
 QY 982 ---RRGP-----PIPKARPPSGRTWAOPGYKPKPLXGK----- 1011
 DB 937 LLPRGRLGVRAKTRKTSERSQPRGRQPIPKARPPSGRTWAOPGYKPKPLXGK----- 996
 QY 1012 ---DRRSTGKSWGKPGYFVPRKTKRN 1034
 DB 997 WLLSPRGRPSWFGPTD---FRRSRN 1019

RESULT 8

AAR68547

ID AAR68547 standard; protein; 841 AA.

XX AC AAR68547;

XX DT 25-MAR-2003 (revised)

DT 17-AUG-1995 (first entry)
 XX HCV protease/hSOD fusion protein expression vector cflSODp600.
 DE
 XX
 XX Hepatitis C virus protease/hSOD fusion protein; HCV;
 KW expression vector cflSODp600; viral infectivity inhibition.
 XX
 OS Hepatitis C virus.
 XX
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..155
 FT /label= SOD leader
 XX
 XX US5371017-A.
 XX
 XX
 PD 06-DEC-1994.
 XX
 XX 04-APR-1991; 91US-00680296.
 XX
 XX 04-APR-1990; 90US-00505433.
 XX (CHIR) CHIRON CORP.
 XX
 XX Houghton M, Choo Q, Kuo G;
 XX
 XX WPI; 1995-021889/03.
 DR N-PSDB; AAQ80175.
 XX
 XX DNA encoding hepatitis C virus protease - used to produce large amts. of
 PT the protease and to develop prods. for inhibition of viral infectivity.
 XX
 XX Claim 10; Fig 10; 69pp; English.
 XX
 XX AAQ80175 (which encodes AAR68547) describes the sequence of the hepatitis
 CC C virus (HCV) protease/hSOD fusion protein E. coli expression vector.
 CC cflSODp600. Other claimed HCV protease fusion partners are yeast alpha-
 CC factor, IL-2S, ubiquitin, beta-galactosidase, beta-lactamase, horseradish
 CC peroxidase, glucose oxidase and urease. The HCV protease fusion proteins
 CC can be used in the production of Abs. They can also be used for assaying
 CC agents which inhibit protease activity, to identify compounds which
 CC inhibit viral infectivity. (Updated on 25-MAR-2003 to correct PF field.)
 XX
 XX Sequence 841 AA;
 SQ

Query Match 51.6%; Score 3050.5; DB 2; Length 841;
 Best Local Similarity 72.6%; Pred. No. 3.6e-206;
 Matches 615; Conservative 10; Mismatches 37; Indels 185; Gaps 11;

QY 1 MATKAVCVLKGDGPVQGIINFEKESNGPVPKWSIKGLTEGLHGFHVFHFGDNTAGCTS 60
 DB 1 MATNPVCVLKGDGPVQGIINFEKESNGPVPKWSIKGLTEGLHGFHVFHFGDNTAGCTS 60
 QY 61 AGPHENPLSRKHGPKDEERHVGDLGNVTADKGVADVSTEDSVISLGDHCHIGRLTVV 120
 DB 61 PGPHFNPLSRKHGPKDEERHVGDLGNVTADKGVADVSTEDSVISLGDHCHIGRLTVV 120
 QY 121 HEKADDLGKGGNEESTKTGNAGSRLACGVIGIAQNLNSGNCISYFCHITGHR----- 173
 DB 121 HEKADDLGKGGNEESTKTGNAGSRLACGVIGIRR-----IGTVVY-NHLTFLRDWAHNGL 174
 QY 174 -----NAWKLGSA-----RTTSGFVS----- 190
 DB 175 RDLAVAVEPVVFSQMETKLTITWADTAACGIINGLPVSARRGREILLGPADGVSKGWR 234
 QY 191 LFAP-----GAKQNRTH-----VTG 205
 DB 235 LLAPITAYAOQTRGLLCITITSLTRDKNQVEGVQIVSTAAQTFLATCIINGVCWTYYH 294
 QY 206 GAAART-----TSGLT----- 216
 DB 295 GAGTRTITASPKGPVIQMTYNTVDQLVGPASQGRTRSLTPTCTGSSDLVLTVRHADVIPVR 354
 QY 217 -----SLFSP-----GAS-----QNTQLIVDFIPVENLET 241

DB 355 RRGDSRGLLSPRPISYLKSSGGELLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLET 414
 QY 242 TMRSPVFTDSSPPVVPQSFQVAHLHAPTGSKSTKPAAYAAQGYKVLNPSVAATLG 301
 DB 415 TMRSPVFTDSSPPVVPQSFQVAHLHAPTGSKSTKPAAYAAQGYKVLNPSVAATLG 474
 QY 302 FGAYMSKAHGIDPNIRTVGRTITTTGSPITYSTYGYFLADGGCGGAYDIIICDECHSTDA 361
 DB 475 FGAYMSKAHGIDPNIRTVGRTITTTGSPITYSTYGYFLADGGCGGAYDIIICDECHSTDA 534
 QY 362 TSILGIGTVLDOAETAGARLVLATATPPGVTVPHPNIEEVALSTTGIPYGYKAIPLE 421
 DB 535 TSILGIGTVLDOAETAGARLVLATATPPGVTVPHPNIEEVALSTTGIPYGYKAIPLE 594
 QY 422 VIKGGRHLIFCHSKKKKDELAALKVALGINAVAYYRGDLVSVIPTSGDVVVVATDALMTG 481
 DB 595 VIKGGRHLIFCHSKKKKDELAALKVALGINAVAYYRGDLVSVIPTSGDVVVVATDALMTG 654
 QY 482 YTGDFDSVIDCNTCVTVDFSLDPTFTIETITLFDQAVSRTQRRGRTGRGPGIYRFVA 541
 DB 655 YTGDFDSVIDCNTCVTVDFSLDPTFTIETITLFDQAVSRTQRRGRTGRGPGIYRFVA 714
 QY 542 PGERPSPGMDSSVLCEDYDAGCAWYELTEAETTVRLRAYMNTPEGLPVCODHLEFWEGVET 601
 DB 715 PGERPSPGMDSSVLCEDYDAGCAWYELTEAETTVRLRAYMNTPEGLPVCODHLEFWEGVET 774
 QY 602 GLTHIDAHELSQTSKSGENLPYLVAQATVCARAQAPPESWDQMKCLIRLKPTHLGPTP 661
 DB 775 GLTHIDAHELSQTSKSGENLPYLVAQATVCARAQAPPESWDQMKCLIRLKPTHLGPTP 834
 QY 662 LLYRLGA 668
 DB 835 LLYRLGA 841

RESULT 9
 ABO27020
 ID ABO27020 standard; protein; 841 AA.
 XX
 AC ABO27020;
 XX
 DT 09-SEP-2003 (first entry)
 XX
 DE Hepatitis C virus (HCV) protease associated vector cflSODp600.
 XX
 KW Hepatitis C virus; HCV; protease; protease inhibition; viral infection;
 KW enzyme.
 XX
 OS Synthetic.
 XX
 XX US2003027317-A1.
 XX
 PD 06-FEB-2003.
 XX
 XX 18-JUN-2001; 2001US-00884456.
 PF
 XX 04-APR-1990; 90US-00505433.
 PR 04-APR-1991; 91US-00680296.
 PR 06-DEC-1994; 94US-00350884.
 PR 12-MAY-1995; 95US-0040548.
 PR 06-SEP-1996; 96US-00709177.
 PR 19-FEB-1999; 99US-00253230.
 XX
 (HOUG/) HOUGHTON M.
 PA (CHOO/) CHOO Q.
 PA (KUOG/) KUO G.
 XX
 XX Houghton M, Choo Q, Kuo G;
 XX
 XX WPI; 2003-492037/58.
 DR N-PSDB; ACDA4796.
 XX

CC useful in assaying and designing antiviral agents specific for HCV. The
 CC method is used in identifying antiviral agents effective for treating
 CC HCV. The present sequence is an HCV protease/hSOD fusion protein.
 XX
 SQ Sequence 841 AA;
 Query Match 51.6%; Score 3050.5; DB 7; Length 841;
 Best Local Similarity 72.6%; Pred. No. 3.6e-206;
 Matches 615; Conservative 10; Mismatches 37; Indels 185; Gaps 11;
 QY 1 MATKAVCVLKGDGPVQGIINFEOKESNGPVKWSIKGLTEGLHGFVHEFGDNTAGCTS 60
 DB 1 MATNPVCVLKGDGPVQGIINFEOKESNGPVKWSIKGLTEGLHGFVHEFGDNTAGCTS 60
 QY 61 AGPHFNPLSRKHGPKDEERHVGDLGNVTADKGVADVSIEDSVLSGDHCHIIIGRTLTV 120
 DB 61 PGPHFNPLSRKHGPKDEERHVGDLGNVTADKGVADVSIEDSVLSGDHCHIIIGRTLTV 120
 QY 121 HEKADDLGKGNEESTKTGNAGSLACGVIGIAQNLNGCNCISYIPGHITGHR----- 173
 DB 121 HEKADDLGKGNEESTKTGNAGSLACGVIGIRR-----IGTYVY-NHLTPLRDMAHNL 174
 QY 174 -----MAKLGSA-----RTTSGFVS----- 190
 DB 175 RDLAVAVEPVVFSQMETKLITWGADTAACGDIINGLPVSARRGRIILGPADGMVSKGWR 234
 QY 191 LFAP-----GAKONETH-----VTG 205
 DB 235 LLAPITAYAAQTRGLLGCIIITSLTGDKNOVEGEVQIVSTAQTFLATCIINGVCWTVVH 294
 QY 206 GAAART-----TSGLT----- 216
 DB 295 GAGTRTIASPKGPIQMTNVQDLVGPASQGRSLTPTCTGSSDLXLVTRHADVIPVR 354
 QY 217 -----SLFSP-----GAS-----QNIQLIVDRIPVENLET 241
 DB 355 RRGDSRGLSLRPISYLGSSGGPLLCAGHAGVIFRAAVCTRGVAKAVDRIPVENLET 414
 QY 242 TWRSVPFTDNSPPVVPQSFQVAHLHAPTSGKSTKVPAAAYAAQGVKVLNPSVAATLG 301
 DB 415 TWRSVPFTDNSPPVVPQSFQVAHLHAPTSGKSTKVPAAAYAAQGVKVLNPSVAATLG 474
 QY 302 FGAYMSKAHGDINIRTVRTITTTGSPITYSTYVTKFLADGGCGGAYDIIICDECHSTDA 361
 DB 475 FGAYMSKAHGDINIRTVRTITTTGSPITYSTYVTKFLADGGCGGAYDIIICDECHSTDA 534
 QY 362 TSILGIGTVLDQAEAGARLVLATATPPGSVTVPHNTEEVALSTTGETIPRYGKALPLE 421
 DB 535 TSILGIGTVLDQAEAGARLVLATATPPGSVTVPHNTEEVALSTTGETIPRYGKALPLE 594
 QY 422 VIKGGRHLIFCHSKKKDELAALKVALGINAVAYRGLDVSIVPTSGDVVVVATDALTMTG 481
 DB 595 VIKGGRHLIFCHSKKKDELAALKVALGINAVAYRGLDVSIVPTSGDVVVVATDALTMTG 654
 QY 482 YTGDFDVIDNCNTCVTQVDFSLDPTFTTITILPQDAVSRTORRGTRGKGGIYRFA 541
 DB 655 YTGDFDVIDNCNTCVTQVDFSLDPTFTTITILPQDAVSRTORRGTRGKGGIYRFA 714
 QY 542 PGRPSGMDFFSVLCECYDAGCWAYELTFAETTVRLRAYMNTPLPVCODHLEFSGVFT 601
 DB 715 PGRPPGMDFSSVLCEDYDAGCWAYELTFAETTVRLRAYMNTPLPVCODHLEFSGVFT 774
 QY 602 GLTHIDAHFLSQTQKSGENLPYLVAQATVCARAQAPPSPDQWKKLIRLKLPTLHGPTP 661
 DB 775 GLTHIDAHFLSQTQKSGENLPYLVAQATVCARAQAPPSPDQWKKLIRLKLPTLHGPTP 834
 QY 662 LLYRLGA 668
 DB 835 LLYRLGA 841

ID AAW01701 standard; protein; 841 AA.
 XX AC AAW01701;
 XX DT 17-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 03-APR-1997 (first entry)
 XX hSOD-HCV fusion protein.
 XX HCV; NS3; non-structural domain 3; protease; polyprotein; inhibitor;
 KW screen; processing; infection; treatment; probe; hepatitis C virus.
 KW Homo sapiens.
 OS Chimeric.
 PH Key Location/Qualifiers
 FT Protein 156..841
 FT /label= HCV_protease
 XX US5585258-A.
 PN 17-DEC-1996.
 XX 06-DEC-1994; 94US-00350884.
 PF 04-APR-1990; 90US-00505433.
 PR 04-APR-1991; 91US-00680296.
 XX (CHIR) CHIRON CORP.
 PA Choo Q, Kuo G, Houghton M;
 PI WPI; 1997-051175/05.
 DR N-PSDB; AAT59261.
 XX Compens. contg. hepatitis C virus NS3 domain protease and related fusion
 PT proteins - useful for screening specific inhibitors, potential antiviral
 PT agents, pregn. of antibodies and for cleaving specific poly:peptide(s).
 XX Example 4; Col 77-84; 68pp; English.
 XX Compens. comprising the hepatitis C virus (HCV) NS3 domain protease or
 CC its active truncation analogues are claimed. Also new are fusion proteins
 CC comprising the protease (or analogues) and, e.g. human superoxide (SOD)
 CC or ubiquitin. The protease is essential for polyprotein processing, and
 CC thus infectivity, in HCV. The compens. are used to screen for specific
 CC inhibitors (possibly useful as antiviral agents), to generate specific
 CC antibodies and to cleave specific polypeptides. HCV cDNA clones (AAT59250
 CC - 56 encoding AAW01686-92 resp.) were isolated from HCV genomic library
 CC using probes AAT59244-49. The clones were used in the preparation of full
 CC -length SOD-protease fusion proteins. The present sequence is encoded by
 CC vector cflSODp600 which contains a full-length HCV protease coding
 CC sequence fused to a functional hSOD leader. The resulting vector encodes
 CC amino acids 1-151 of hSOD, and amino acids 946-1630 of HCV (corresponding
 CC to 1-686 of AAW01693). (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 17-OCT-2003 to standardise OS field)
 XX Sequence 841 AA;
 SQ
 Query Match 51.5%; Score 3047.5; DB 2; Length 841;
 Best Local Similarity 72.6%; Pred. No. 5.9e-206;
 Matches 615; Conservative 9; Mismatches 38; Indels 185; Gaps 11;
 QY 1 MATKAVCVLKGDGPVQGIINFEOKESNGPVKWSIKGLTEGLHGFVHEFGDNTAGCTS 60
 DB 1 MATNPVCVLKGDGPVQGIINFEOKESNGPVKWSIKGLTEGLHGFVHEFGDNTAGCTS 60
 QY 61 AGPHFNPLSRKHGPKDEERHVGDLGNVTADKGVADVSIEDSVLSGDHCHIIIGRTLTV 120
 DB 61 PGPHFNPLSRKHGPKDEERHVGDLGNVTADKGVADVSIEDSVLSGDHCHIIIGRTLTV 120

QY 121 HEKADDLKGGNEESTKTGNAGSLACGVIGIAQNLSGNCSTIYPGHITGHR-----173
Db |||||
QY 121 HEKADDLKGGNEESTKTGNAGSLACGVIGIR-----GTVVY-NHLTPLRDWAHGL 174
174 |||||-----MAWKLGSAA-----RTSGFVS-----190
Db 175 RDLAVAVEPVFSQMETKLITWGADTAACGDIINGLPVSARRGRILLGPADGMVSKGWR 234
QY 191 LFAP-----GAKQNEH-----VTG 205
Db 235 LLAPITAYAAQTRGLLGCIIITSLTGRDKNOVEGEVQIVSTAQTFLATCIINGVCWTVH 294
QY 206 GAAART-----TSGLT-----216
Db 295 GAGTRTIASPKGPVIQWYTNVDQDLVGWPASQGTSLTPTCTCGSSDLYLVRHADVIPVR 354
QY 217 -----SLFSP-----CAS-----217
Db 355 RRGDSRGLSPRIPIVYKSGSGPILCPAGHAGVIFRAAVCTRGVAKAVDFIPVENLET 414
QY 242 TMRSPVFTDNSSPPVVPQSFQVAHLHAPTSGSKTKVPAAYAAQYKVLVLPNSVAATLG 301
Db 415 TMRSPVFTDNSSPPVVPQSFQVAHLHAPTSGSKTKVPAAYAAQYKVLVLPNSVAATLG 474
QY 302 FGAYMSKAHGIDPNIRTGVRTITGSPITYSYGKFLADGGCGGAYDIIICDECHSTDA 361
Db 475 FGAYMSKAHGIDPNIRTGVRTITGSPITYSYGKFLADGGCGGAYDIIICDECHSTDA 534
QY 362 TSIIGIGVLDQAEATAGARLVLAATPPGSVTVVPHNIEEVALSTTGEIPFYKAIPL 421
Db 535 TSIIGIGVLDQAEATAGARLVLAATPPGSVTVVPHNIEEVALSTTGEIPFYKAIPL 594
QY 422 VIKGRHLIFCHSKKKDELAAKLVALGINAVAYRGLDVSIVPTSGDWWVATDALTG 481
Db 595 VIKGRHLIFCHSKKKDELAAKLVALGINAVAYRGLDVSIVPTSGDWWVATDALTG 654
QY 482 YTGDFDSVIDNCTVQTVDLSLPTFTIETITPQDAVSTQRRGTRGKPGIYRFA 541
Db 655 YTGDFDSVIDNCTVQTVDLSLPTFTIETITPQDAVSTQRRGTRGKPGIYRFA 714
QY 542 PGERPSGMFSSVLCECYDAGCAWYELTPAETTVLRAYMNTPGIPVODHLEFWEVFT 601
Db 715 PGERPSGMFSSVLCECYDAGCAWYELTPAETTVLRAYMNTPGIPVODHLEFWEVFT 774
QY 602 GLTHIDAHFLSQTKSGENLPYLVAQATVCARAQAPPPSDQWKKLIRLKPILHGPTP 661
Db 775 GLTHIDAHFLSQTKSGENLPYLVAQATVCARAQAPPPSDQWKKLIRLKPILHGPTP 834
QY 662 LLYRLGA 668
Db 835 LLYRLGA 841

RESULT 12

AAW46397
ID AAW46397 standard; protein; 841 AA.

AC AAW46397;

DT 27-AUG-2003 (revised)

TX 07-MAY-1998 (first entry)

DE Amino acid sequence of the vector cf1SODp600.

XX Protease; HCV; NS3 domain; human superoxide dismutase; fusion protein;
XX assay; activity; anti-HCV.

OS Synthetic.

OS Hepatitis C virus.

XX Homo sapiens.

XX US5712145-A.

PD 27-JAN-1998.
XX 06-SEP-1996; 96US-00709173.
XX 04-APR-1990; 90US-00505433.
PR 04-APR-1991; 91US-00680296.
PR 06-DEC-1994; 94US-00350884.
PR 12-MAY-1995; 95US-00440548.
XX (CHIR) CHIRON CORP.
XX Choo Q, Kuo G, Houghton M;
PI WPI: 1998-111986/11.
XX N-PSDB; AAV04993.
DR Recombinant hepatitis C virus protease - useful in screening drugs for
PT activity against hepatitis C virus.
XX Disclosure; Fig 10A-G; 68pp; English.
XX The present sequence represents the amino acid sequence of the vector
CC cf1SODp600. This vector contains a full length Hepatitis C virus (HCV)
CC protease coding sequence fused to a functional human superoxide dismutase
CC leader. The vector was used to express the protease fusion protein in
CC Escherichia coli. The HCV protease is believed to cleave itself from the
CC genomic polyprotein. In the absence of protease activity, the HCV
CC polyprotein should remain in its unprocessed form, and thus render the
CC virus non-infectious. Inhibitors of protease activity should also inhibit
CC viral infectivity. The protease can therefore be used for assaying
CC compounds for activity against HCV. (Updated on 27-AUG-2003 to correct OS
XX field.)
SQ Sequence 841 AA;
Query Match 51.5%; Score 3047.5; DB 2; Length 841;
Best Local Similarity 72.6%; Pred. No. 5.9e-206;
Matches 615; Conservative 9; Mismatches 38; Indels 185; Gaps 11;
QY 1 MATKAVCVLKDGVPQGIINFEQKESNGPVKVMGSIKGLTEGLGHFVHEFGDNTAGCTS 60
Db |||||
QY 1 MATNPVCVLKDGVPQGIINFEQKESNGPVKVMGSIKGLTEGLGHFVHEFGDNTAGCTS 60
61 AGPHFNPLSRKHGPKDRERHVGDLGNVTADKGVADVSIEDSVISLSDGHCIIIGRTLV 120
Db 61 PGPHFNPLSRKHGPKDRERHVGDLGNVTADKGVADVSIEDSVISLSDGHCIIIGRTLV 120
QY 121 HEKADDLKGGNEESTKTGNAGSLACGVIGIAQNLSGNCSTIYPGHITGHR-----173
Db 121 HEKADDLKGGNEESTKTGNAGSLACGVIGIR-----GTVVY-NHLTPLRDWAHGL 174
QY 174 -----MAWKLGSAA-----RTSGFVS-----190
Db 175 RDLAVAVEPVFSQMETKLITWGADTAACGDIINGLPVSARRGRILLGPADGMVSKGWR 234
QY 191 LFAP-----GAKQNEH-----VTG 205
Db 235 LLAPITAYAAQTRGLLGCIIITSLTGRDKNOVEGEVQIVSTAQTFLATCIINGVCWTVH 294
QY 206 GAAART-----TSGLT-----216
Db 295 GAGTRTIASPKGPVIQWYTNVDQDLVGWPASQGTSLTPTCTCGSSDLYLVRHADVIPVR 354
QY 217 -----SLFSP-----CAS-----217
Db 355 RRGDSRGLSPRIPIVYKSGSGPILCPAGHAGVIFRAAVCTRGVAKAVDFIPVENLET 414
QY 242 TMRSPVFTDNSSPPVVPQSFQVAHLHAPTSGSKTKVPAAYAAQYKVLVLPNSVAATLG 301
Db 415 TMRSPVFTDNSSPPVVPQSFQVAHLHAPTSGSKTKVPAAYAAQYKVLVLPNSVAATLG 474
QY 302 FGAYMSKAHGIDPNIRTGVRTITGSPITYSYGKFLADGGCGGAYDIIICDECHSTDA 361
Db |||||

Db 475 FGAYMSKAHGIDPNIRTVGRTITTSPTITSTYTKFLADGGCGGAYDIIICDECHSTDA 534
 QY 362 TSILGIGTVLDOAETAGARLVLAATATPPGSVTVPHNIEEVALSTTGEIIPFYKAIPL 421
 Db 535 TSILGIGTVLDOAETAGARLVLAATATPPGSVTVPHNIEEVALSTTGEIIPFYKAIPL 594
 QY 422 VIKGGRHLIFCHSKKCDLAALVALGINAVAYYRGDLVSVIPTSGLVVDVATDALMTG 481
 Db 595 VIKGGRHLIFCHSKKCDLAALVALGINAVAYYRGDLVSVIPTSGLVVDVATDALMTG 654
 QY 482 YTGDFSDVIDCNTCTVTQTVDFSLDPTFTTETITLPODAVSRTORRGTRGKPGIYRFA 541
 Db 655 YTGDFSDVIDCNTCTVTQTVDFSLDPTFTTETITLPODAVSRTORRGTRGKPGIYRFA 714
 QY 542 PGERPSGMFDSVLCEDYDAGCAWYELTAPETTVRLRAYMNTPLPVCODHLEFWEVFT 601
 Db 715 PGERPSGMFDSVLCEDYDAGCAWYELTAPETTVRLRAYMNTPLPVCODHLEFWEVFT 774
 QY 602 GLTHIDAHFLSQTQSGENLPYLVAQATVCARAQAPPPSDQMWKCLIRLPTLHGPTP 661
 Db 775 GLTHIDAHFLSQTQSGENLPYLVAQATVCARAQAPPPSDQMWKCLIRLPTLHGPTP 834
 QY 662 LLYRLGA 668
 Db 835 LLYRLGA 841

RESULT 13

AAW97609
 ID AAW97609 standard; protein; 841 AA.

XX AAW97609;

AC 26-MAY-1999 (first entry)

XX Amino acid sequence of vector cflSODp600.

XX HCV NS3 protease; truncation analog; HCV control; protease activity;
 KW viral infectivity; inactive non-cleaving protease.

XX Synthetic.

OS Hepatitis C virus.

XX US5885799-A.

XX 23-MAR-1999.

XX 06-SEP-1996; 96US-00709177.

XX 04-APR-1990; 90US-00505433.

PR 04-APR-1991; 91US-00680296.

PR 06-DEC-1994; 94US-00350884.

PR 12-MAY-1995; 95US-004040548.

XX (CHIR) CHIRON CORP.

XX Choo Q, Kuo G, Houghton M;

XX WPI; 1999-228536/19.

DR N-PSDB; AAX26398.

XX Preparation of new Hepatitis C Virus NS3 protease - useful for screening
 for compounds which inhibit HCV infectivity.

XX Example 3; Fig 10; 71pp; English.

XX The specification describes a method for making a purified Hepatitis C
 virus (HCV) NS3 protease or active truncation analog. If the HCV protease
 C N-terminal cleavage signal is excluded (so that self-cleavage is
 prevented), the HCV protease remains in its unprocessed form, and renders
 the virus noninfectious. The protease is therefore useful for assaying
 CC pharmaceutical agents for control of HCV, as compounds which inhibit
 CC protease activity sufficiently will also inhibit viral infectivity. An

CC inactive non-cleaving protease can be used to screen for inhibitors.
 CC Recombinant expression systems can be utilised to prepare recombinant HCV
 CC which can be used to produce monoclonal antibodies. The present sequence
 CC was created in the course of the invention

XX SQ Sequence 841 AA;

Query Match 51.5%; Score 3047.5; DB 2; Length 841;
 Best Local Similarity 72.6%; Pred. No. 5.9e-206;
 Matches 615; Conservative 9; Mismatches 38; Indels 185; Gaps 11;

QY 1 MATKAVCVLKGDPVQGIINFEQESNGPVKVGSIKGLTEGLHGFHVHEFDNTAGCTS 60
 Db 1 MAINPVCVLKGDPVQGIINFEQESNGPVKVGSIKGLTEGLHGFHVHEFDNTAGCTS 60
 QY 61 AGPHFNPLSRKHGGPKDEERHVGDIGNVTADKGVADVSIEDSVISLSDHCIIIGRTLVV 120
 Db 61 PGPHFNPLSRKHGGPKDEERHVGDIGNVTADKGVADVSIEDSVISLSDHCIIIGRTLVV 120
 QY 121 HEKADDLKGGNEESTKTNAGSRLACGVIGTGAQNLSGNCNCIYPGHITGHR----- 173
 Db 121 HEKADDLKGGNEESTKTNAGSRLACGVIGIR-----GTIVY-NHLTPLRDWAHNL 174
 QY 174 -----MAWKLGSAA-----RTTSGFVS----- 190
 Db 175 RDLAVAVEPVFSQMETKLIITWGAADTAACDIIINGLIPVSARRGREILLGPADGMVSKWR 234
 QY 191 LFAP-----GAKQNETH-----VTG 205
 Db 235 LLAPITAYAQOTRGLLGIITSLTGRDKNQVEGEVQIVSTAAQTFLATCIINGVCTVYH 294
 QY 206 GAAART-----TSGLT----- 216
 Db 295 GAGTRTIASPKGEVIQMTNVQDLVGMWPAASQTRSLTPTCTCGSSDLXIVTRHADVIPVR 354
 QY 217 -----SLFSP-----GAS-----QNTQLIVDFIPVENLET 241
 Db 355 RRGDSRGLLSRPISYILKSGSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLET 414
 QY 242 TMRSPVFTDNSSPPVVPVQSFQVAHLHAPTGSKSTKVPAAAYAAQGYKVLVLPNSVAATLG 301
 Db 415 TMRSPVFTDNSSPPVVPVQSFQVAHLHAPTGSKSTKVPAAAYAAQGYKVLVLPNSVAATLG 474
 QY 302 FGAYMSKAHGIDPNIRTVGRTITTSPTITSTYTKFLADGGCGGAYDIIICDECHSTDA 361
 Db 475 FGAYMSKAHGIDPNIRTVGRTITTSPTITSTYTKFLADGGCGGAYDIIICDECHSTDA 534
 QY 362 TSILGIGTVLDOAETAGARLVLAATATPPGSVTVPHNIEEVALSTTGEIIPFYKAIPL 421
 Db 535 TSILGIGTVLDOAETAGARLVLAATATPPGSVTVPHNIEEVALSTTGEIIPFYKAIPL 594
 QY 422 VIKGGRHLIFCHSKKCDLAALVALGINAVAYYRGDLVSVIPTSGLVVDVATDALMTG 481
 Db 595 VIKGGRHLIFCHSKKCDLAALVALGINAVAYYRGDLVSVIPTSGLVVDVATDALMTG 654
 QY 482 YTGDFSDVIDCNTCTVTQTVDFSLDPTFTTETITLPODAVSRTORRGTRGKPGIYRFA 541
 Db 655 YTGDFSDVIDCNTCTVTQTVDFSLDPTFTTETITLPODAVSRTORRGTRGKPGIYRFA 714
 QY 542 PGERPSGMFDSVLCEDYDAGCAWYELTAPETTVRLRAYMNTPLPVCODHLEFWEVFT 601
 Db 715 PGERPSGMFDSVLCEDYDAGCAWYELTAPETTVRLRAYMNTPLPVCODHLEFWEVFT 774
 QY 602 GLTHIDAHFLSQTQSGENLPYLVAQATVCARAQAPPPSDQMWKCLIRLPTLHGPTP 661
 Db 775 GLTHIDAHFLSQTQSGENLPYLVAQATVCARAQAPPPSDQMWKCLIRLPTLHGPTP 834
 QY 662 LLYRLGA 668
 Db 835 LLYRLGA 841

RESULT 14

```

AAR14349
ID AAR14349 standard; protein; 840 AA.
XX
AC AAR14349;
XX
DT 16-JAN-1992 (first entry)
XX
DE HCV protease::hSOD leader fusion encoded by cfISODp600.
XX
KW Hepatitis C virus; HCV; human superoxide dismutase; SOD.
XX
OS Hepatitis C virus.
XX
FH Key
FT Region
FT 1..156
FT Protein
FT 157
FT /label= truncated HCV protease
XX
FN WO9115596-A.
XX
PD 17-OCT-1991.
XX
PF 04-APR-1990; 90US-00505434.
XX
PR 04-APR-1990; 90US-00505434.
XX
PA (PROT-) PROTOS INC.
XX
PI Rosenberg S;
XX
DR WPI; 1991-325236/44.
XX
DR N-PSDB; AAR14358.
XX
PT Method for assaying pharmaceutical cpds. - for determining anti-Hepatitis
PT C Virus activity, using binding affinity.
XX
PS Example 4; Fig 10; 68pp; English.
XX
CC The vector cfISODp600 contains a full-length HCV protease coding sequence
CC fused to a functional hSOD leader. The truncated protease analogue
CC expressed by the vector is proteolytically inactive and can be used to
CC assay a wide range of pharmaceutical agents for controlling HCV. Those
CC agents which inhibit the protease activity sufficiently will also inhibit
CC viral infectivity. See also AAR14350-R14356
XX
SQ Sequence 840 AA;

Query Match          51.5%; Score 3042.5; DB 2; Length 840;
Best Local Similarity 72.6%; Pred. No. 1.3e-205;
Matches 614; Conservative 9; Mismatches 38; Indels 185; Gaps 11;

QY 2 ATKAVCVLKGDPVQGIINFQKSNQPKVYWGSIKGLTEGLHGFHVEFGDNTAGCTSA 61
DB 1 ATNFCVCLKGDPVQGIINFQKSNQPKVYWGSIKGLTEGLHGFHVEFGDNTAGCTSP 60
QY 62 GPHENPLSRKHGPKDEERHVGDLGNVTADKGVADVSIEDSVLSGDHCHIIIGRTLVVH 121
DB 61 GPHENPLSRKHGPKDEERHVGDLGNVTADKGVADVSIEDSVLSGDHCHIIIGRTLVVH 120
QY 122 EKADDLKGKGNESRTKTGNAGSRACGVIGTAQNLNSGNCNCSITYPGHITGHR----- 173
DB 121 EKADDLKGKGNESRTKTGNAGSRACGVIGIR-----GTIVY-NHLTPLRDWAHNGLR 174
QY 174 -----MAWKLGSAA-----RTTSGFVS-----L 191
DB 175 DLAVAVEPVVFSQMETKLTWGAUTACGDIINGLPVSRARGREILLGPADGMVSKGNRL 234
QY 192 FAP-----GAKQNEH-----VTGG 206
DB 235 LAPITAVAQOTRGLGCIITSLTRDKNQVGEVQIVSTAAQTFLATCIINGVCMVYHG 294
QY 207 AARFT-----TSLGT----- 216

```

23

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 21, 2004, 10:18:09 ; Search time 49.4736 Seconds
(without alignments)
4734.482 Million cell updates/sec

Title: US-10-658-782-4
Perfect score: 4455
Sequence: 1 MATKAVCVLKGDPVQGIIN.....GNKRRRTGSKWGKPGYPMP 829

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4455	100.0	829	AAE18690	Multiple
2	4455	100.0	829	ADC06769	Chimeric
3	4032	90.5	1099	AUJ76378	HCV multi
4	4032	90.5	1099	ABG72262	HCV multi
5	2222	49.9	1021	AW34481	HCV antig
6	2222	49.9	1021	AAW40039	Fusion pr
7	2222	49.9	1021	AAE22050	PSOP/c200
8	1627.5	36.5	1766	AAE22041	Hepatitis
9	1624.5	36.5	2261	AAE90164	Peptide e
10	1624.5	36.5	2436	AAE92050	Sequence
11	1624.5	36.5	2436	AAE90288	Peptide e
12	1624.5	36.5	2772	AAE18540	Protein e
13	1624.5	36.5	2955	AAE14975	Amino aci
14	1624.5	36.5	2955	AAE18541	Polyprote
15	1624.5	36.5	3011	AAE21519	Compiled
16	1624.5	36.5	3011	AAE90931	Hepatitis
17	1624.5	36.5	3011	AAW34480	HCV polyp
18	1624.5	36.5	3011	AAW40038	HCV polyp
19	1624.5	36.5	3011	AAE22049	Hepatitis
20	1623	36.4	781	AAE22208	Sequence
21	1623	36.4	781	AAE21565	HCV CKS-3
22	1623	36.4	781	AAE33632	HCV CKS-3
23	1623	36.4	781	AAE33594	HCV CKS-3
24	1623	36.4	781	AAE33574	HCV CKS-3
25	1623	36.4	781	AAE52690	HCV CKS-3

26	1623	36.4	781	4	AAE51372	HCV recom
27	1622.5	36.4	3011	5	AAU84597	HCV polyp
28	1621.5	36.4	2301	1	AAE92047	Sequence
29	1621.5	36.4	2772	2	AAE08123	Hepatitis
30	1619.5	36.4	2894	2	AAE24440	Composite
31	1616.5	36.3	2816	2	AAE34009	HCV-1 pol
32	1615.5	36.3	2435	2	AAE25135	HCV polyp
33	1614.5	36.2	2894	2	AAE70230	Composite
34	1614.5	36.2	3011	2	AAE31621	Hepatitis
35	1608.5	36.1	2436	2	AAE28582	HCV amino
36	1605.5	36.0	1786	1	AAE90158	Protein s
37	1600.5	35.9	2955	2	AAE08124	Hepatitis
38	1597.5	35.9	2202	6	AAE26783	Protein d
39	1597.5	35.9	2631	6	AAE26785	Protein d
40	1597.5	35.9	2984	4	AAE00442	Hepatitis
41	1597.5	35.9	3011	2	AAE40120	HCV genom
42	1597.5	35.9	3011	2	AAE77397	Hepatitis
43	1597.5	35.9	3011	2	AAE77398	Hepatitis
44	1597.5	35.9	3011	2	AAE98021	Infectiou
45	1597.5	35.9	3011	2	AAE98020	Infectiou

ALIGNMENTS

RESULT 1
AAE18690
ID AAE18690 standard; protein; 829 AA.
XX
AC AAE18690;
XX
DT 17-MAY-2002 (first entry)
XX
DE Multiple epitope fusion antigen (MEFA) 12 protein.
XX
KW Hepatitis C virus; NS3/4a antigen; multiple epitope fusion antigen;
KW HCV infection; MEFA 12 protein.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Misc-difference 315 /note= "Encoded by ATG"
FT Misc-difference 645 /note= "Encoded by GAG"
XX
PN WO200196875-A2.
XX
PD 20-DEC-2001.
XX
14-JUN-2001; 2001WO-US019369.
XX
15-JUN-2000; 2000US-0212082P.
PR 02-APR-2001; 2001US-0280811P.
PR 02-APR-2001; 2001US-0280867P.
XX
(CHIR) CHIRON CORP.
XX
Chien DY, Arcangel P, Tandeske L, George-Nascimento C, Coit D;
Medina-Selby A;
WPI; 2002-179522/23.
N-PSDB; AAD29796.
XX
Immunoassay solid support useful for detecting hepatitis C virus
infection in a biological sample, comprises at least one of HCV anti-core
antibody and HCV NS3/4a epitope, bound to the support.
XX
Disclosure; Fig 7; 87pp; English.
XX
The present invention relates to hepatitis C virus (HCV) core antigen and
NS (nonstructural) 3/4a antibody combination assay that can detect both
HCV antigens and antibodies present in a sample using a single solid

CC matrix as well as immunoassay solid supports for use in the assay. The
CC solid support is useful for detecting HCV infection in a biological
CC sample. The present sequence is MEFA (multiple epitope fusion antigen) 12
CC protein. This sequence is used in the exemplification of the invention
XX
SQ Sequence 829 AA;
Query Match 100.0%; Score 4455; DB 5; Length 829;
Best Local Similarity 100.0%; Pred. No. 1.7e-310; Mismatches 0; Indels 0; Gaps 0;
Matches 829; Conservative 0;
QY 1 MATKAVCVLKGDPVQGIINFEQKESNGPVKVGSIKGLTEGLGHFVHEFGDNTAGCTS 60
DB 1 MATKAVCVLKGDPVQGIINFEQKESNGPVKVGSIKGLTEGLGHFVHEFGDNTAGCTS 60
QY 61 AGPHFNPLSTRGCNCSIYPGHITGHRMAWKLGSAAARTTSGFVSLFAPGAKQNETHVTTGGA 120
DB 61 AGPHFNPLSTRGCNCSIYPGHITGHRMAWKLGSAAARTTSGFVSLFAPGAKQNETHVTTGGA 120
QY 121 AARTTSGLTSLFSPGASONIQLITSDNSPPVQSFQVAHLHAPTGSKSTKVPAAAYA 180
DB 121 AARTTSGLTSLFSPGASONIQLITSDNSPPVQSFQVAHLHAPTGSKSTKVPAAAYA 180
QY 181 AQQYKVLVLPNSVAATLGFAGYMSKAHGIDPNIRIGVTRITTTGSPITYSTYKFLADGGC 240
DB 181 AQQYKVLVLPNSVAATLGFAGYMSKAHGIDPNIRIGVTRITTTGSPITYSTYKFLADGGC 240
QY 241 SGGAYDIIICDECHSTDATSLIGTGLDQABTAGARLVLAATPPGSGVTVPHPNIEEV 300
DB 241 SGGAYDIIICDECHSTDATSLIGTGLDQABTAGARLVLAATPPGSGVTVPHPNIEEV 300
QY 301 ALSTGTGEPFVGKAIPELVKGGRHLLFCHSKKCDLAAKLVALGINAVAYRGLDVSV 360
DB 301 ALSTGTGEPFVGKAIPELVKGGRHLLFCHSKKCDLAAKLVALGINAVAYRGLDVSV 360
QY 361 IPTSGDVVVATDALMTGYTDFDSDVIDCNTCAGSKPAIIPDREVLVYREFDEMECSQH 420
DB 361 IPTSGDVVVATDALMTGYTDFDSDVIDCNTCAGSKPAIIPDREVLVYREFDEMECSQH 420
QY 421 LPYTEQGMMLAEQFKQKALGSRGKPAIVDPKELVYQOYDEMECSQAAYIEQAQVIA 480
DB 421 LPYTEQGMMLAEQFKQKALGSRGKPAIVDPKELVYQOYDEMECSQAAYIEQAQVIA 480
QY 481 HOFKEKVLGLDNDQVVVTPDKELLYEAFDEMECSKAALIEGORMAEMLKSKIQGLL 540
DB 481 HOFKEKVLGLDNDQVVVTPDKELLYEAFDEMECSKAALIEGORMAEMLKSKIQGLL 540
QY 541 GILRRHVGPGEQAVQWMNRLIAFASRGNHVSPTHYVPSRRRFAQALPVWARPDPNPLV 600
DB 541 GILRRHVGPGEQAVQWMNRLIAFASRGNHVSPTHYVPSRRRFAQALPVWARPDPNPLV 600
QY 601 ETWKKPDYEPVHVGRSSRRFAQALPVWARPDPNPLVETWKKPDYEPVHVGRKTKENT 660
DB 601 ETWKKPDYEPVHVGRSSRRFAQALPVWARPDPNPLVETWKKPDYEPVHVGRKTKENT 660
QY 661 NRRPDQVFPGGQIVGGVILLPRRGPRLGLVLAATKTSPIPKARPEGRWTAQPGYPWPL 720
DB 661 NRRPDQVFPGGQIVGGVILLPRRGPRLGLVLAATKTSPIPKARPEGRWTAQPGYPWPL 720
QY 721 YGNKDRSTGSKGKPGVPWPRKTRNNRPPQDVKFFGGQIVGGVILLPRRGPRLGLV 780
DB 721 YGNKDRSTGSKGKPGVPWPRKTRNNRPPQDVKFFGGQIVGGVILLPRRGPRLGLV 780
QY 781 ATRKTSPIPKARPEGRWTAQPGYPWPLVYGNKDRSTGSKGKPGYPW 829
DB 781 ATRKTSPIPKARPEGRWTAQPGYPWPLVYGNKDRSTGSKGKPGYPW 829
RESULT 2
ADC06769
ID ADC06769 standard; protein; 829 AA.
XX
AC ADC06769;

XX 18-DEC-2003 (first entry)
DT Chimeric multiple epitope fusion antigen 12 protein.
DE immunoassay solid support; HCV; NS3/4a; non-structural;
XX non-A, non-B hepatitis; NANB; multiple epitope fusion antigen 12; MEFA12;
KW chimeric.
XX Chimeric.
OS Synthetic.
OS Unidentified.
OS Hepatitis C virus.
OS Homo sapiens.
XX US2002192639-A1.
EN 19-DEC-2002.
XX 14-JUN-2001; 2001US-00881239.
XX 15-JUN-2000; 2000US-0212082P.
PR 02-APR-2001; 2001US-0280811P.
PR 02-APR-2001; 2001US-0280867P.
XX (CHIE/) CHIEN D Y.
PA (ARCA/) ARCANGEL P.
PA (TAND/) TANDESKE L.
PA (GEOR/) GEORGE-NASCIMENTO C.
PA (COIT/) COIT D.
PA (MEDI/) MEDINA-SELBY A.
XX Chien DY, Arcangel P, Tandeske L, George-Nascimento C, Coit D;
PI Medina-Selby A;
PI WPI; 2003-644609/61.
DR N-PSDB; ADC06770.
XX Immunoassay solid support for detecting hepatitis C virus infection in
PT biological samples, comprises a hepatitis C virus anti-core antibody and
PT an isolated hepatitis C virus NS3/4a epitope bound HCV anti-core
PT antibody.
XX Claim 45; Fig 7; 40pp; English.
PS The invention relates to a novel immunoassay solid support comprising at
XX least one hepatitis C virus (HCV) anti-core antibody and at least one
CC isolated HCV NS3/4a (non-structural protein 3/4a) epitope bound thereto.
CC The system of the invention may be useful for detecting HCV infection in
CC a biological sample and for treating or detecting non-A, non-B hepatitis
CC (NANB hepatitis). The current sequence is that of the chimeric multiple
CC epitope fusion antigen 12 (MEFA12) protein of the invention.
XX Sequence 829 AA;
SQ Query Match 100.0%; Score 4455; DB 7; Length 829;
Best Local Similarity 100.0%; Pred. No. 1.7e-310;
Matches 829; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATKAVCVLKGDPVQGIINFEQKESNGPVKVGSIKGLTEGLGHFVHEFGDNTAGCTS 60
DB 1 MATKAVCVLKGDPVQGIINFEQKESNGPVKVGSIKGLTEGLGHFVHEFGDNTAGCTS 60
QY 61 AGPHFNPLSTRGCNCSIYPGHITGHRMAWKLGSAAARTTSGFVSLFAPGAKQNETHVTTGGA 120
DB 61 AGPHFNPLSTRGCNCSIYPGHITGHRMAWKLGSAAARTTSGFVSLFAPGAKQNETHVTTGGA 120
QY 121 AARTTSGLTSLFSPGASONIQLITSDNSPPVQSFQVAHLHAPTGSKSTKVPAAAYA 180
DB 121 AARTTSGLTSLFSPGASONIQLITSDNSPPVQSFQVAHLHAPTGSKSTKVPAAAYA 180
QY 181 AQQYKVLVLPNSVAATLGFAGYMSKAHGIDPNIRIGVTRITTTGSPITYSTYKFLADGGC 240

Db 181 AQQYKVLNPNVAATLGFAYMSKAHGDIDPNIRTCVRIITTTGSPITYSTYKGLADGGC 240
 QY 241 SGGAVDIIICDECHSTDATSIILGIGVLDQAEATAGARLVVLTATATPPGSGVTVPHNIEV 300
 Db 241 SGGAVDIIICDECHSTDATSIILGIGVLDQAEATAGARLVVLTATATPPGSGVTVPHNIEV 300
 QY 301 ALSTTGEIPFYGKAIPLEVIKGRHLIFCHSKKCDLAALVALGINAVAYRGLDVS 360
 Db 301 ALSTTGEIPFYGKAIPLEVIKGRHLIFCHSKKCDLAALVALGINAVAYRGLDVS 360
 QY 361 IPTSGDVVVVATDALMTGTYGDFDSVIDCNTCAGSGKPAIIPDREVLVREFDEMECSOH 420
 Db 361 IPTSGDVVVVATDALMTGTYGDFDSVIDCNTCAGSGKPAIIPDREVLVREFDEMECSOH 420
 QY 421 LPYIEQGMMLAQFQKALGLSRGKPAIVPKDEVLYQYDEMECSQAAPYIEQAQVIA 480
 Db 421 LPYIEQGMMLAQFQKALGLSRGKPAIVPKDEVLYQYDEMECSQAAPYIEQAQVIA 480
 QY 481 HOPKEKVLGIDNDQVVVTPDKELLYEAFDEMECSKKAALTEGORMAEMLSKIQGLL 540
 Db 481 HOPKEKVLGIDNDQVVVTPDKELLYEAFDEMECSKKAALTEGORMAEMLSKIQGLL 540
 QY 541 GILRRHVGEGAVQWNNRLIAFASRGHVSPTHYVPSRRRFAQALPVWARPDYNPPLV 600
 Db 541 GILRRHVGEGAVQWNNRLIAFASRGHVSPTHYVPSRRRFAQALPVWARPDYNPPLV 600
 QY 601 ETWKKPDYPPVHGSSRRRFAQALPVWARPDYNPPLVETWKKPDYPPVHGSRKTKRNT 660
 Db 601 ETWKKPDYPPVHGSSRRRFAQALPVWARPDYNPPLVETWKKPDYPPVHGSRKTKRNT 660
 QY 661 NRRPDVFPGGGOIVGGVYLPARGPLGLVATKTSPIPKARRPGEHTWAPGYPWPL 720
 Db 661 NRRPDVFPGGGOIVGGVYLPARGPLGLVATKTSPIPKARRPGEHTWAPGYPWPL 720
 QY 721 YGNKDRRSTGKSGKPGYPPWPKTKRNTNRRPQDVKFGGQIVGGVYLPARGPLGLV 780
 Db 721 YGNKDRRSTGKSGKPGYPPWPKTKRNTNRRPQDVKFGGQIVGGVYLPARGPLGLV 780
 QY 781 ATRKTSPIPKARRPGEHTWAPGYPWPLYGNKDRRSTGKSGKPGYPWP 829
 Db 781 ATRKTSPIPKARRPGEHTWAPGYPWPLYGNKDRRSTGKSGKPGYPWP 829
 RESULT 3
 AAU76378
 ID AAU76378 standard; protein; 1099 AA.
 XX
 AC AAU76378;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE HCV multiple epitope fusion antigen (MEFA) 7.1 protein sequence.
 XX
 KW Hepatitis C virus; HCV; NS3/4a conformational epitope; seroconversion;
 KW immunoassay solid support; multiple epitope fusion antigen; MEFA;
 KW non-structural protein.
 XX
 OS Hepatitis C virus.
 OS Synthetic.
 XX
 PN WO200196870-A2.
 XX
 PD 20-DEC-2001.
 XX
 XX 14-JUN-2001; 2001WO-US019156.
 PF
 XX
 PR 15-JUN-2000; 2000US-0212082P.
 PR
 PR 02-APR-2001; 2001US-0280811P.
 PR
 XX 02-APR-2001; 2001US-0280867P.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PI Chien DY, Arcangel P, Tandeske L, George-Nascimento C, Coit D;

PI Medina-Selby A;
 XX
 DR WPI; 2002-090228/12.
 DR N-PSDB; ABX15345.
 XX
 PT Immunoassay solid support, useful for detecting hepatitis C virus
 PT infection in biological sample, comprises HCV NS3/4a conformational
 PT epitope and multiple epitope fusion antigen bound to the support.
 XX
 PS Claim 5; Fig 5; 92pp; English.
 XX
 CC The present invention relates to a new immunoassay solid support
 CC consisting essentially of at least one hepatitis C virus (HCV) NS3/4a
 CC conformational epitope and a multiple epitope fusion antigen (MEFA),
 CC bound to the support. The NS3/4a conformational epitope and/or MEFA
 CC reacts specifically with anti-HCV antibodies present in a biological
 CC sample from an HCV-infected individual. The immunoassay of the invention
 CC is useful for detecting hepatitis C virus infection in a biological
 CC sample. The method of the invention provides a sensitive, accurate
 CC diagnostic and prognostic tool to provide adequate patient care and to
 CC prevent transmission of HCV by blood and by blood products, or by
 CC personal contact. Use of NS3/4a conformational epitope in combination
 CC with MEFA, provides a sensitive and reliable method for detecting early
 CC HCV seroconversion. Use of MEFA has the added advantages of decreasing
 CC masking problems, improving sensitivity in detecting antibodies by
 CC allowing a greater number of epitopes on a unit surface area of
 CC substrate, and improving substrate. Detection accuracy is increased and
 CC the incidence of false results is reduced because of the identification
 CC and the use of highly immunogenic HCV antigens which are present during
 CC the early stages of HCV seroconversion. The present amino acid sequence
 CC represents the multiple epitope fusion antigen (MEFA) 7.1 of the
 CC invention
 XX
 SQ Sequence 1099 AA;
 Query Match 90.5%; Score 4032; DB 5; Length 1099;
 Best Local Similarity 69.8%; Pred. No. 5.4e-280;
 Matches 791; Conservative 1; Mismatches 3; Indels 338; Gaps 7;
 QY 1 MATKAVCVLKGDPVQGIINFEQESNGFVKVWSIKGLTEGLHGFVHFEFDNTAGCTS 60
 Db 1 MATKAVCVLKGDPVQGIINFEQESNGFVKVWSIKGLTEGLHGFVHFEFDNTAGCTS 60
 QY 61 AGPHENPLSTR----- 71
 Db 61 AGPHENPLSRKHGPKDBERHVGDLGNVTADKGVADVSIEDSVLSGDHCIIGRTLTV 120
 QY 72 -----GCNCSIYFGHITGHRMAWKLS 93
 Db 121 HEKADDLKGGNESTKYNAGSRLACGVIGTAQNLNSGCNCSIYFGHITGHRMAWKLS 180
 QY 94 AARTTSGFVSLFAPGAKQNETHTVGTGAARTTSGTSLFSPGASQNIQLITS----- 145
 Db 181 AARTTSGFVSLFAPGAKQNETHTVGTGAARTTSGTSLFSPGASQNIQLIVDFIPVENLE 240
 QY 146 -----TDNSPPVFPQSFQVAHLHAPTGSKSTKVPAAQYKVLNPNVAATL 197
 Db 241 TTMRSPVFTDNSSPPVFPQSFQVAHLHAPTGSKSTKVPAAQYKVLNPNVAATL 300
 QY 198 GFGAYMSKAHGDIDPNIRTCVRIITTTGSPITYSTYKGLADGGSGGAYDIIICDECHSTD 257
 Db 301 GFGAYMSKAHGDIDPNIRTCVRIITTTGSPITYSTYKGLADGGSGGAYDIIICDECHSTD 360
 QY 258 ATSLIGIGTVLDQAEATAGARLVVLTATATPPGSGVTVPHNIEVALSTTGEIPFYKAIPL 317
 Db 361 ATSLIGIGTVLDQAEATAGARLVVLTATATPPGSGVTVPHNIEVALSTTGEIPFYKAIPL 420
 QY 318 EVIKGGRHLIFCHSKKCDLAALVALGINAVAYRGLDVSIVPTSGDVVVVATDALMT 377
 Db 421 EVIKGGRHLIFCHSKKCDLAALVALGINAVAYRGLDVSIVPTSGDVVVVATDALMT 480
 QY 378 GYTGDFDSVIDCNTC----- 392

Db 481 GYTGDFDVIDNCTCVTQTVDLSLDPFTTITLPQDAVSRTQRRGKRGKPGIYRFV 540
 Qy 393 ----- 392
 Db 541 APGERPSGMFDSVLCYDAGCAWYELTTPAETTVRLRAYMNTPLGFPVQDHLFWEQVF 600
 Qy 393 ----- 392
 Db 601 TGLTHIDAHFLSQTKSGENLPYLVAQAVCARAQAPPSWDQWKKLIRLKLTLHGPT 660
 Qy 393 ----- 416
 Db 661 PLLYRLGAVQNEITLTHPVTKYIMTCMSADLEVVTSSACSGKPAIIPDREVLYREFDEMEE 720
 Qy 417 CSQHLPIEQGMMLAEQFKQKALGSRGGKPAIIVDPKVELYQOYDEMECSQAAPYIEQA 476
 Db 721 CSQHLPIEQGMMLAEQFKQKALGSRGGKPAIIVDPKVELYQOYDEMECSQAAPYIEQA 780
 Qy 477 QVIAHQFKEKVLGLINDQVVVTPDKELLYEAFDEMEECASKAALIEBQGQMAEMLKSKI 536
 Db 781 QVIAHQFKEKVLGLINDQVVVTPDKELLYEAFDEMEECASKAALIEBQGQMAEMLKSKI 840
 Qy 537 QGLLGILRRHVGPGEQAVQWNNRLIAPASRGNHVSPTHYVPSRRRFAQALPVVWARPDYN 596
 Db 841 QGLLGILRRHVGPGEQAVQWNNRLIAPASRGNHVSPTHYVPSRRRFAQALPVVWARPDYN 900
 Qy 597 PPLVETWKKPDYEPVHVGRSSRRFAQALPVVWARPDYNPLVETWKKPDYEPVHVGRKT 656
 Db 901 PPLVETWKKPDYEPVHVGRSSRRFAQALPVVWARPDYNPLVETWKKPDYEPVHVGRKT 960
 Qy 657 KRNTNRPPQDVKFGGGQIVGGVLLPRGPRGLGLATKTSPIPKARRPGRTWAOQGY 716
 Db 961 KRNTNRPPQDVKFGGGQIVG-----RRGP-----PIPKARRPGRTWAOQGY 1003
 Qy 717 PWPYLGKDRRSTCKSGKPGYWPRTKRNTRNPQDVKFGGGQIVGGVLLPRGRPR 776
 Db 1004 PWPYLGKDRRSTCKSGKPGYWPRTKRNTRNPQDVKFGGGQIVG-----RRGP- 1056
 Qy 777 LGVLATKTSPIPKARRPGRTWAOQGYWPYLYGNKDRSRGKSGKPGYWP 829
 Db 1057 -----PIPKARRPGRTWAOQGYWPYLYGNKDRSRGKSGKPGYWP 1099

RESULT 4
 ID ABG72262
 XX ABG72262 standard; protein; 1099 AA.
 AC ABG72262;
 XX
 DT 06-MAR-2003 (first entry)
 XX
 DE HCV multiple epitope fusion antigen 7.1 (MEFA 7.1).
 XX
 KW Immunoassay solid support; Hepatitis C Virus type-1; HCV-1; HCV-2;
 KW NS3/4a conformational epitope; multiple epitope fusion antigen 7.1;
 KW MEFA 7.1; anti-HCV antibody; NS3/4a conformational antigen; HCV-3;
 KW HCV infection; Hepatitis C Virus type-2; Hepatitis C Virus type-3;
 KW mutant; mutin.
 XX
 OS Hepatitis C virus type 1.
 OS Hepatitis C virus type 2.
 OS Hepatitis C virus type 3.
 OS Synthetic.
 OS Chimeric.
 XX
 FH Key
 FT Region
 FT 1. .156
 FT /note= "Correspond to amino acids 1-156 of HCV-1 NSOD
 FT superoxide dismutase")
 FT 159. .176
 FT /note= "Correspond to amino acids 303-320 of HCV-1 E1"
 FT 179. .199
 FT /note= "Correspond to consensus sequence of amino acids
 FT

FT 390-410 of HCV-1 E2 HVR"
 FT 200. .230
 FT /note= "Correspond to consensus sequence of amino acids
 FT 384-414 of HCV-1 and HCV-2 E2 HVR"
 FT 231. .696
 FT /note= "Correspond to amino
 FT acids 1193-1658 of HCV-1
 FT helicase"
 FT 699. .745
 FT /note= "Correspond to amino
 FT acids 1689-1735 of HCV-1 5-1-
 FT 1 epitope"
 FT 748. .794
 FT /note= "Correspond to amino
 FT acids 1689-1735 of HCV-3 5-1-
 FT 1 epitope"
 FT 797. .843
 FT /note= "Correspond to amino
 FT acids 1689-1735 of HCV-2 5-1-
 FT 1 epitope"
 FT 846. .881
 FT /note= "Correspond to amino
 FT polypeptide C100"
 FT 884. .919
 FT /note= "Correspond to amino
 FT acids 2278-2313 of HCV-1 NS5
 FT region"
 FT 922. .957
 FT /note= "Correspond to amino
 FT acids 2278-2313 of HCV-1 NS5
 FT region"
 FT 958. .1028
 FT /note= "Correspond to core region antigenic determinants
 FT from amino acids 9-32, 39-42 and 64-88 of HCV-1 and amino
 FT acids 67-84 of HCV-2"
 FT 1029. .1099
 FT /note= "Correspond to core region antigenic determinants
 FT from amino acids 9-32, 39-42 and 64-88 of HCV-1 and amino
 FT acids 67-84 of HCV-2"
 XX
 US2002146685-A1.
 XX 10-OCT-2002.
 XX 14-JUN-2001; 2001US-00881654.
 XX 15-JUN-2000; 2000US-0212082P.
 PR 02-APR-2001; 2001US-0280811P.
 PR 02-APR-2001; 2001US-0280867P.
 XX (CHIE//) CHIEN D Y.
 PA (ARCA//) ARCANDEL P.
 PA (TAND//) TANDESKE L.
 PA (GEOR//) GEORGE-NASCIMENTO C.
 PA (COIT//) COIT D.
 PA (MEDI//) MEDINA-SELBY A.
 XX
 Chien DY, Arcangel P, Tandeske L, George-Nascimento C, Coit D;
 Medina-Selby A;
 WPI; 2003-147573/14.
 N-PSDB; ABX14411.
 XX
 Immunoassay solid support for detecting Hepatitis C Virus infection in
 biological samples, comprises Hepatitis C Virus conformational epitope
 and multiple epitope fusion antigen.
 Claim 25; Fig 5A-5F; 45pp; English.
 XX
 The present invention relates to immunoassays comprising Hepatitis C
 virus (HCV) NS3/4a conformational epitope and multiple epitope fusion
 antigen (MEFA), bound to a solid support. The NS3/4a epitope and/or the
 multiple epitope fusion antigen react with anti-HCV antibodies present in
 a biological sample from an HCV-infected individual. The immunoassays and
 methods of the invention are useful for detecting HCV infection in a
 biological sample. The inventive immunoassay solid support provides a
 sensitive and reliable method for detecting early HCV seroconversion. The
 assays can detect HCV infection caused by any six known genotypes of HCV.
 The use of the multiple epitope fusion proteins decreases masking

CC problems, improves sensitivity in detecting antibodies by allowing a
CC greater number of epitopes on a unit area of substrate, and improves
CC selectivity. The present sequence represents HCV multiple epitope fusion
CC antigen 7.1 (MEFA 7.1), a mutant HCV polypeptide derived from various
CC regions of HCV type 1, 2, or 3 (HCV-1, HCV-2, or HCV-3) polypeptide
CC sequences
XX
SQ Sequence 1099 AA;
Query Match 90.5%; Score 4032; DB 6; Length 1099;
Best Local Similarity 69.8%; Pred. No. 5.4e-280;
Matches 791; Conservative 1; Mismatches 3; Indels 338; Gaps 7;
QY 1 MATKAVCVLKGDPVQGIINFEKQSGNGPVKVGSIKGLTEGLHGHVHPEGDNAGTCS 60
Db 1 MATKAVCVLKGDPVQGIINFEKQSGNGPVKVGSIKGLTEGLHGHVHPEGDNAGTCS 60
QY 61 AGPHENPLSTR----- 71
Db 61 AGPHENPLSRKHGGPKDEERHVDLGNVTADKGVADVSIEDSVLSGDHCIIIGRTLTV 120
QY 72 -----GCNGSIYPGHITGHRMAWKLS 93
Db 121 HEKADDLGKGGNEESTKTGNAGSLACGVIGIAQNLSGNCNSIYPGHITGHRMAWKLS 180
QY 94 AARTSGFVSLPAPGAKQNEHTVGTGAARTSGLTSLFSPGASQNIQLITS----- 145
Db 181 AARTTSGFVSLPAPGAKQNEHTVGTGAARTSGLTSLFSPGASQNIQLIVDFIPVENLE 240
QY 146 -----TDNSSPPVPPQSFQVAVHHAFTGSKSTKVPAAVAAQYKVLVLPNSVAATL 197
Db 241 TTMRSPTVTDNSSPPVPPQSFQVAVHHAFTGSKSTKVPAAVAAQYKVLVLPNSVAATL 300
QY 198 GFGYMSKAHGIDPNIRTVGRTITTSPTITYGKFLADGCGSGGAYDIIICDECHSTD 257
Db 301 GFGYMSKAHGIDPNIRTVGRTITTSPTITYGKFLADGCGSGGAYDIIICDECHSTD 360
QY 258 ATSILIGITVLDQETAGARLVVLTATPPGVSVPVHPNIEVALSTTGEIIFYKAIPL 317
Db 361 ATSILIGITVLDQETAGARLVVLTATPPGVSVPVHPNIEVALSTTGEIIFYKAIPL 420
QY 318 EVIKGRHLIFCHSKKKDELAAKLVGINAVAYRGLDVSIVPTSGDVVVVATDALMT 377
Db 421 EVIKGRHLIFCHSKKKDELAAKLVGINAVAYRGLDVSIVPTSGDVVVVATDALMT 480
QY 378 GYTGFDSVIDNCTC----- 392
Db 481 GYTGFDSVIDNCTCVTQTVDFSLDPTFTIETITLPQDAVSRTQRRGTGRGKGIYRFV 540
QY 393 ----- 392
Db 541 AFGERPFGMFDSSVLCCEYDAGCAMELYLPAETTVLRAYMNTPLGLVCQDHLFEWGVF 600
QY 393 ----- 392
Db 601 TGLTHIDAHFLSQTQSGENLPYLVAIYQVTCARAQAPPPSDQMWKCLIRLKPTLHGFT 660
QY 393 -----ACSGKPAIIPDREVLYREFDEMBE 416
Db 661 PLLYRLGAVONEITLTHPVTKYIMTCSADLEVWTSACSGKPAIIPDREVLYREFDEMBE 720
QY 417 CSQHLPYIEQGMMLARQFKQKALGLSRGKPAIVDPKEVLYQOYDMECSQAAPYIEQA 476
Db 721 CSQHLPYIEQGMMLARQFKQKALGLSRGKPAIVDPKEVLYQOYDMECSQAAPYIEQA 780
QY 477 QVIAHQFKEKVLGLINDQVVTTPDKEILYEADEFDEMEECASKAALIEEGORMAELMSKI 536
Db 781 QVIAHQFKEKVLGLINDQVVTTPDKEILYEADEFDEMEECASKAALIEEGORMAELMSKI 840
QY 537 QGLGLILRRHVHGEGAVQWMNRLIAFASRGNHVSPTHYVPSRRTFAQALPVWARPDPYN 596
Db 841 QGLGLILRRHVHGEGAVQWMNRLIAFASRGNHVSPTHYVPSRRTFAQALPVWARPDPYN 900

QY 597 PPLVETWKKPDYEPVPHGSRRTFAQALPVWARPDPYNPPLVETWKKPDYEPVPHGRT 656
Db 901 PPLVETWKKPDYEPVPHGSRRTFAQALPVWARPDPYNPPLVETWKKPDYEPVPHGRT 960
QY 657 KNTNRRPQDVKFGGQIIVGGVLLPRRPRGLVLAATKTSPIPKARRPEGRRTWAQPGY 716
Db 961 KNTNRRPQDVKFGGQIIVGGVLLPRRPRGLVLAATKTSPIPKARRPEGRRTWAQPGY 1003
QY 717 PMPYGNKDRRSTGKSGKPGYPWPRTKRNTRNPQDVKFGGQIIVGGVLLPRRGR 776
Db 1004 PMPYGNKDRRSTGKSGKPGYPWPRTKRNTRNPQDVKFGGQIIVGGVLLPRRGR 1056
QY 777 LGVLATKTSPIPKARRPEGRRTWAQPGYPWPPLYGNKDRRSTGKSGKPGYPWP 829
Db 1057 -----PIPKARRPEGRRTWAQPGYPWPPLYGNKDRRSTGKSGKPGYPWP 1099
RESULT 5
AAW34481
ID AAW34481 standard; protein; 1021 AA.
XX
AC AAW34481;
DT 25-MAR-2003 (revised)
DT 16-MAR-1998 (first entry)
XX
DE HCV antigen combination pSOD/c200/core.
KW PCR primer; amplify; HCV; hepatitis C virus; antigen combination; NS3;
KW C domain; S domain; NS5; HCV polypeptide; anti-HCV antibody; detection;
KW NS4.
OS Hepatitis C virus.
OS Synthetic.
XX
EH Key Location/Qualifiers
FT Misc-difference 1..902 /note= "linker"
FT Misc-difference 1..154 /note= "hsOD fragment"
FT Misc-difference 155..159 /note= "linker"
FT Misc-difference 160..899 /note= "c200 (amino acids 1192-1931 of HCV polypeptide)"
FT Misc-difference 903..1021 /note= "c22 (amino acids 2-120 of HCV polypeptide)"
XX
XX US5683864-A.
XX
XX 04-NOV-1997.
XX
XX 07-JUL-1992; 92US-00910760.
XX
XX 18-NOV-1987; 87US-00122714.
XX 30-DEC-1987; 87US-00139886.
XX 26-FEB-1988; 88US-00161072.
XX 06-MAY-1988; 88US-00191263.
XX 26-OCT-1988; 88US-00263584.
XX 14-NOV-1988; 88US-00271450.
XX 17-MAR-1989; 89US-00325338.
XX 20-APR-1989; 89US-00341334.
XX 21-APR-1989; 89US-00353896.
XX 18-MAY-1989; 89US-00355002.
XX 04-APR-1990; 90US-00504352.
XX (CHIR) CHIRON CORP.
XX
XX Kuo G, Houghton M, Choo Q;
XX
XX WPI; 1997-548976/50.
XX DR N-PSDB; AAT99982.
XX
XX Combination of three hepatitis C virus antigens - used for detection of
FT

PT specific antibodies to diagnose infection.

XX Example 6; Col 59-68; 57pp; English.

CC This sequence represents a Hepatitis c virus (HCV) antigen combination of
CC the invention. The HCV antigen combination comprises an antigen (Ag1)
CC comprising the C domain (i.e. amino acids (aa) 1-120 of the HCV
CC polyprotein), or its immunologically reactive fragment containing at
CC least 8 aa. It also comprises two additional antigens from two different
CC polyprotein domains, including at least 8 aa from the NS3, NS4, S or NS5
CC domains of the polyprotein, corresponding, respectively, to aa 1050-1640;
CC 1640-2000; 120-400 and 2000-3011 of the HCV polyprotein. Alternatively,
CC Ag1 contains at least 8 aa from the 1-122 or 9-177 aa regions of the HCV
CC polyprotein. These antigen combinations are used diagnostically to detect
CC anti-HCV antibodies, using any standard immunoassay format. These antigen
CC combinations have a broader range of reactivity with antibodies than any
CC antigen individually. (Updated on 25-MAR-2003 to correct PR field.)

XX Sequence 1021 AA;

Query Match 49.9%; Score 2222; DB 2; Length 1021;

Best Local Similarity 46.2%; Pred. No. 3e-150;

Matches 512; Conservative 35; Mismatches 111; Indels 450; Gaps 22;

QY 1 MATKAVCVLKGDPVQGIINFEQKESGPKVWGSIKGLTEGLHGFVHERGDNAGTCTS 60
DB 1 MATKAVCVLKGDPVQGIINFEQKESGPKVWGSIKGLTEGLHGFVHERGDNAGTCTS 60
QY 61 AGPHFNPLSTRGCNCSYIPGHITGHRMAWLKLSAARTSG-----FVSL----- 104
DB 61 AGPHFNPLSRK-----HGPKDEERHVGDLGNVADKGVADVSIEDSVLSLGDHCII 114
QY 105 -----FAPGAKQNEHTVTGGAAATTSGLTSLFSPGASNIQ----- 141
DB 115 GRTLVVHEKADDLGKGNEESTK-TGNAGSLACGVI-----GIAQNLFGADVPIPVEN 168
QY 142 LIITS-----TDNSPPVPOFVAHLHAPTSGSKSTKPAAYAAQYKVLVLPNSVAA 195
DB 169 LETTMRSPVFTDNSSPPVPOFVAHLHAPTSGSKSTKPAAYAAQYKVLVLPNSVAA 228
QY 196 TLGFGAYMSKAHGDIPNIRTVRTITGSPITYSTYKFLADGGCSGAYDIIICDECHS 255
DB 229 TLGFGAYMSKAHGDIPNIRTVRTITGSPITYSTYKFLADGGCSGAYDIIICDECHS 288
QY 256 TDATSIIGIGTVLQAEFAGARLVLTATATPPGVTVPHPNIEVALSTTGEIPFYGKAI 315
DB 289 TDATSIIGIGTVLQAEFAGARLVLTATATPPGVTVPHPNIEVALSTTGEIPFYGKAI 348
QY 316 PLEVIKGRHLIFCHSKKKCDELAALVALGINAVAYRGLDVSIVPTSGDVVVVATDAL 375
DB 349 PLEVIKGRHLIFCHSKKKCDELAALVALGINAVAYRGLDVSIVPTSGDVVVVATDAL 408
QY 376 MTGVTGDFDSVIDCNC----- 392
DB 409 MTGVTGDFDSVIDCNCVTQTVDLSDFPTFTIETITLPQDAVSRQRRGTGRGKPGIYR 468
QY 393 ----- 392
DB 469 FVAPGERPSGDFSSVLCEDACANWELTPAETTVRLRAYMNTPGIPLVCQDHFLEWEG 526
QY 393 ----- 392
DB 529 VFTGLTHIDAHFLSGTKSGENLPVLVAYQATVCARAQAPPPSWDQWKKLRLKPTLHG 588
QY 393 ----- 392
DB 589 PTPLLYRLGAVQNEITITHPVTKYIMTCMSADLEVTVTWVLVGVIAALAAAYCLSTGCV 648
QY 393 -----ACSGKPAIPDREVLRYRFDMEECQHLPYIEQGMALAEQFKQKALGL-----S 442
DB 649 VIVGRVLSGKPAIPDREVLRYRFDMEECQHLPYIEQGMALAEQFKQKALGLQTAS 708
QY 443 RGGKPAIVDPKEVLYQQYD-----EMEECSQAAPYIEQAQVIAHQFKEKVLGLINDQVW 497

DB 709 ROAE-VIAPAVQTNQXLETFWAKHWMNFISGIQYLAGLSLPG--NPALIASLMAFTAAV 765
QY 498 VTP---DKELIYE-----AFDEMEBCASKAALIEECQRMVLMKSKIQ 537
DB 766 TSPLTTSTQLLENTLNGWVAQAALAPGAATAFVAGLAGAIGSVGLGKVLIDILAGYGA 825
QY 538 GLLG-----ILRRHVGPGEAGVOMN 558
DB 826 GVAGALVAFKIMSEVSTEDLVNLLPAILSPGALVGVVCAAILRRHVGEAGVOMN 885
QY 559 RLIAFASGRGHVSTHYVPSRRAQALPVWAREDPYNPLVETWKKPDYEPVPPVHGSRSS 618
DB 886 RLIAFASGRGHVSP-----GNSS 903
QY 619 RRFQAALPVWARPDPYNPLVETWKKPDYEPVPPVHGRTKRTNRRPQDVKPPGGQIVGG 678
DB 904 T-----NP-----KPO-----KKNKNTNRRPQDVKPPGGQIVGG 934
QY 679 VYLLPRGPRGLGLATRKTS-----PIKARRPEGRTWAQPGYPWPPLYGNK----- 724
DB 935 VYLLPRGPRGLGLATRKTS-----PIKARRPEGRTWAQPGYPWPPLYGNK----- 724
QY 725 -----DRRSTGKSGWKPGYPWPWKTKN 747
DB 995 AGWLLSPRSGRPSMGPTD---PRRRSRN 1019
RESULT 6
AAW40039
ID AAW40039 standard; protein; 1021 AA.
XX AC AAW40039;
XX DT 26-MAY-1998 (first entry)
XX DE Fusion protein c200/c22.
XX KW Hepatitis C virus C domain; HCV; immunological activity; c200/c22;
XX KW NS3 domain; NS4 domain; S domain; NS5 domain; fusion protein.
XX OS Synthetic.
XX OS Hepatitis virus.
XX FN US5712087-A.
XX PD 27-JAN-1998.
XX PF 12-MAY-1995; 95US-00440519.
XX PR 04-APR-1990; 90US-00504352.
XX PR 07-JUL-1992; 92US-00910760.
XX (CHIR) CHIRON CORP.
XX Kuo G, Houghton M, Choo Q;
XX WPI; 1998-119973/11.
XX N-PSDS; AAV09990.
XX Immunoassays for hepatitis C virus antibodies - using combinations of
XX antigenic fragments of HCV polyprotein.
XX Example 6; Fig 4; 59pp; English.
CC This sequence represents a fusion protein constructed from the hepatitis
CC C virus core domain (which is situated at the carboxy terminus of the
CC fusion protein) and a c200 construct (a fusion of the NS3 and NS3
CC domains). This protein used in the construction of novel combinations of
CC HCV antigens that have a broader range of immunological activity than any
CC single HCV antigen. An example of such an antigen given in this
CC specification comprises a first antigen containing at least 8 amino acids
CC of the C domain of the HCV polyprotein and a second antigen comprising at

Qy	619	RRFAQALPFWARPDYNPLVETWTKPDYEPFVWVGRTKRTNTNRPPQDVKFFGGGQIVGG	678
Db	904	T-----NP-----KPQ-----KKKRNTRNRPPQDVKFFGGGQIVGG	934
Qy	679	VYLLPRGPRGLVLTARKTS-----PIPKARREGEGRTWAOGPWPWPLYGNK----	724
Db	935	VYLLPRGPRGLVLTARKTSRSQPRGRQPIPKARREGEGRTWAOGPWPWPLYGNCGCW	994
Qy	725	-----DRRSTGKSWGKPGYPWPWRPKTRN	747
Db	995	AGWLLSPRGSRPSWGPTD---PRRSRN	1019
RESULT 7			
AAE22050	ID	AAE22050 standard; protein; 1021 AA.	
XX	XX	AAE22050;	
XX	DT	16-JUL-2002 (first entry)	
XX	DE	psOD/c200/core expression plasmid protein.	
XX	KW	Hepatitis C virus; HCV; antigen; C domain; polyprotein; NS3 domain;	
XX	KW	NS4 domain; S domain; NS5 domain; psOD/c200/core plasmid.	
XX	OS	Hepatitis C virus.	
XX	OS	Unidentified.	
XX	XX	Chimeric.	
XX	Key	Location/Qualifiers	
FT	Region	1..154	
FT	FT	/note= "hsOD"	
FT	Region	155..159	
FT	FT	/note= "Linker region"	
FT	Region	160..899	
FT	FT	/note= "HCV c200"	
FT	Region	900..902	
FT	FT	/note= "Linker region"	
FT	Region	903..1021	
FT	FT	/note= "HCV c22"	
XX	XX	US6312889-B1.	
XX	XX	06-NOV-2001.	
XX	XX	12-MAY-1995; 95US-00440549.	
XX	XX	04-APR-1990; 90US-00504352.	
XX	XX	07-JUL-1992; 92US-00910760.	
XX	XX	(CHIR) CHIRON CORP.	
XX	XX	Houghton M, Choo Q, Kuo G;	
XX	XX	WPI; 2002-040268/05.	
XX	XX	N-PSDB; AAD35044.	
XX	XX	Combination of hepatitis C viral (HCV) antigens, useful in improved	
XX	XX	immunoassay for detecting HCV antibodies.	
XX	XX	Example 6; Fig 4; 58pp; English.	
XX	CC	The invention relates to combination of hepatitis C viral (HCV) antigens	
XX	CC	that have a broader range of immunological reactivity than any single HCV	
XX	CC	antigen. The combinations consist of an antigen from the C domain of the	
XX	CC	HCV polyprotein, and at least one additional HCV antigen from either the	
XX	CC	NS3 domain, the NS4 domain, the S domain, or the NS5 domain and are in	
XX	CC	the form of fusion protein, a simple physical mixture, or the individual	
XX	CC	antigens commonly bound to a solid matrix. The combinations of antigens	
XX	CC	provides broad range immunoassays for anti-HCV antibodies. The invention	
XX	CC	therefore provides a method for detecting antibodies to HCV in a mammal	

CC suspected of containing such antibodies. The present sequence is a
CC protein encoded by pSOB/c200/core expression plasmid DNA containing HCV
CC coding sequence
XX
SQ Sequence 1021 AA;

Query Match 49.9%; Score 2222; DB 5; Length 1021;
Best Local Similarity 46.2%; Pred. No. 3e-150;
Matches 512; Conservative 35; Mismatches 111; Indels 450; Gaps 22;

QY 1 MATKAVCVLKGDPVQGIINFEQESNGPVKVMGSIKGLTEGLHGFHVEFGDNTAGCTS 60
DB 1 MATKAVCVLKGDPVQGIINFEQESNGPVKVMGSIKGLTEGLHGFHVEFGDNTAGCTS 60

QY 61 AGHFNFPLSTGNCNCTYPGHITGRMAWKLGSARTTSG-----FVSL----- 104
DB 61 AGHFNFPLSRK-----HGGPKDERHVGDIGNVTADKGDVADVSDVSLSDGHCII 114

QY 105 -----FAPGAKONETHVTGGAARTTSGTSLFSPGASONTQ----- 141
DB 115 GRTLVVHEKADDLGKGNEESTK-TGNAGSLACGVI-----GIAQNLEFGAVDFIPVEN 168

QY 142 LITS-----TDNSSPPVWPOSFOVAHLHAPTSGSKSTKVPAAVAAGYKVLVLPNSVAA 195
DB 169 LETTMRSPVFTDSSPPVWPOSFOVAHLHAPTSGSKSTKVPAAVAAGYKVLVLPNSVAA 228

QY 196 TLGFGAYMSKAHGIDPNIRGTITTSPTTYSTYTKGFLADGGCGGAYDIIICDECHS 255
DB 229 TLGFGAYMSKAHGIDPNIRGTITTSPTTYSTYTKGFLADGGCGGAYDIIICDECHS 288

QY 256 TDATSIILGIGTLDQAEATAGARLVVLATATPPGSVTVPHNIEEVALSTTGEIPFYGKAI 315
DB 289 TDATSIILGIGTLDQAEATAGARLVVLATATPPGSVTVPHNIEEVALSTTGEIPFYGKAI 348

QY 316 PLEVIKGGRHLIFCHSKKKCDELAALKVALGINAVYRGLDVSVIPTSGDVVVVATDAL 375
DB 349 PLEVIKGGRHLIFCHSKKKCDELAALKVALGINAVYRGLDVSVIPTSGDVVVVATDAL 408

QY 376 MTGVTGDFSDVIDNCTC----- 392
DB 409 MTGVTGDFSDVIDNCTCQTQVDFSLDPTFTIETITLPQDAVSRTORRGTGRGKPGIYR 468

QY 393 ----- 392
DB 469 FVAPGERPSGMFDSVLCYDAGCANVELTPAETTVLRLAYMNTPGLPVCQDHLFEWEG 528

QY 393 ----- 392
DB 529 VFTGLTHIDAHFLSQTKSGENLPYLVAQATVCARAQAPPPSWDMWKCLIRLKPILHG 588

QY 393 ----- 392
DB 589 PTPLLYRLGAVQNEITLTHPVTKYIMTCMSADLEVTSTWVLVGVLAALAAAYCLSTGCV 648

QY 393 -----ACSGKPAIPDREVLRYREFDEMECSOHLPYIEQGMMLAEQFKALGL-----S 442
DB 649 VIVGRVLSGKPAIPDREVLRYREFDEMECSOHLPYIEQGMMLAEQFKALGLQTA 708

QY 443 RGGKPAIPVPEVLYQQYD-----EMECSSAAYPIEQAVIAHQFKEKVLGLDNDQVV 497
DB 709 RQAE-VIAPAVQTNQKLETFWAKHMWNFISGIQYLAGSLTPG--NPAIASLMAFTA 765

QY 498 VTP-----DKEIIE-----AFDEMEECASKAALIEGORMAEMKSKIQ 537
DB 766 TSPLTTSTQTLLENLIGWVAAQLAAPGRATAFVAGLAGAAGSVGLGKVLIDILAGYGA 825

QY 538 GLLG-----IIRHVGEGEAGVQNMN 558
DB 826 GVAGALVAFKIMSGEVPSTEDLVNLLPAILSPGALVVGWVCAAILRRHVGEGEAGVQNMN 885

QY 559 RLIAFASRGNHVSPTHVPSRSRFAQALPWARNPDYNPPLVETWKKPDYPPVHVGRSS 618
DB 886 RLIAFASRGNHVSP-----GNSS 903

QY 619 RRFAQALPVWARPDPYNDPPLVETWKKPDYEPVPHGRKTKRNTNRRPQDVKFPGGQIVGG 678
DB 904 T-----NP-----KPO-----KKKNTNRRPQDVKFPGGQIVGG 934

QY 679 VYLLPRGPRGLVLAIRKTS-----PIKARRPEGRWTAAQPGVWPPLYGNK----- 724
DB 935 VYLLPRGPRGLVLAIRKTS-----PIKARRPEGRWTAAQPGVWPPLYGNK----- 994

QY 725 -----DRSTGKSGWKGEGYWPAPKTKN 747
DB 995 AGWLLSPRSGRPSWGPTD---PRRSRN 1019

RESULT 8
AAP92041
ID AAP92041 standard; protein; 1766 AA.
XX
AC AAP92041;
DT 25-MAR-2003 (revised)
DT 02-MAR-1990 (first entry)
XX
Hepatitis C virus (HCV) cDNA inserts in clones 14i, 11b, 7f, 7e, 8h, 33c, 40b, 37b, 35, 36, 81, 32, 33b, 25c, 14c, 8f, 33f, 33g and 39c.
DE
XX
Hepatitis C virus (HCV); non-A, non-B hepatitis (HANEH).
KW
XX
Hepatitis C virus.
OS
XX
EP318216-A.
PD 31-MAY-1989.
XX
18-NOV-1988; 88EP-00310922.
PF
XX
18-NOV-1987; 87US-00122714.
PR 30-DEC-1987; 87US-00139886.
PR 26-FEB-1988; 88US-00161072.
PR 06-MAY-1988; 88US-00191263.
PR 26-OCT-1988; 88US-00263584.
PR 14-NOV-1988; 88US-00271450.
XX
(CHIR) CHIRON CORP.
(CHIR) CHIRON CORP.
XX
Houghton M, Choo QL, Kuo G;
XX
WPI; 1989-159274/22.
DR N-PSDB; AAN92097.
XX
Purified hepatitis C virus - and associated nucleic acids and polypeptide(s).
PT
XX
Claim 13; Fig 26-1, 26-2, 26-3, 26-4, 26-5, 26-6; 139pp; English.
XX
It is the sequence encoded in the open reading frame of hepatitis C virus cDNA inserts in clones 14i, 11b, 7f, 7e, 8h, 33c, 40b, 37b, 35, 36, 81, 32, 33b, 25c, 14c, 8f, 33f, 33g and 39c. It is antigenic and could be used in immunoassay reagents and vaccines and to generate antibodies useful in diagnosis and passive immunotherapy for HCV infection/non-A, non-B hepatitis. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PI field.)
CC
XX
SQ Sequence 1766 AA;

Query Match 36.5%; Score 1627.5; DB 1; Length 1766;
Best Local Similarity 36.6%; Pred. No. 2.7e-107;
Matches 398; Conservative 26; Mismatches 81; Indels 581; Gaps 15;

QY 146 TDNSSPPVWPOSFOVAHLHAPTSGSKSTKVPAAVAAGYKVLVLPNSVAAITLFGAYMSK 205
DB 495 TDNSSPPVWPOSFOVAHLHAPTSGSKSTKVPAAVAAGYKVLVLPNSVAAITLFGAYMSK 554

```
QY 206 AHGIDPNIRTVRTITGSPITYSTYKFLADGGCGGAYDIIICDECHSTDATSILGIG 265
Db 555 AHGIDPNIRTVRTITGSPITYSTYKFLADGGCGGAYHIIICDECHSTDATSILGIG 614
QY 266 TVLDQAGTAGARLVLATATPGSVTVPHNPHEEVALSTTGEIPFYGKAIPLEVIKGGRH 325
Db 615 TVLDQAGTAGARLVLATATPGSVTVPHNPHEEVALSTTGEIPFYGKAIPLEVIKGGRH 674
QY 326 LIFCHSKKCCDELAALVALGINAVAYRGDLVSIVPTSGDVVVVATDALTMTGYTGFDS 385
Db 675 LIFCHSKKCCDELAALVALGINAVAYRGDLVSIVPTSGDVVVVATDALTMTGYTGFDS 734
QY 386 VIDCNTC----- 392
Db 735 VIDCNTCVTQTVDFSIDPTFTTITLPODAVSRTOQRGRTGRGKGIYRFVAPGERPSG 794
QY 393 ----- 392
Db 795 MFDSSVLCYDEGCANWYELTPAETTVRLRAYMNTFGLPVCQDHLEFWEGVETGLTHIDA 854
QY 393 ----- 392
Db 855 HFLSOTKQSGENLPYLVAQATWARAQAPPSWDQWKKLIRLKPETHLHGPTPLLYRLGA 914
QY 393 -----ACSG 396
Db 915 VQNEILTHPTKYIMTMSADLEVVTSTVWLVGGVLAALAAAYCLSTGCVWIVGRVVLGS 974
QY 397 KPAILPDREVLVREDFEMECCSHLPYIIOGWMLABQFKQKALGL- ---SRGKPAIVPD 452
Db 975 KPAILPDREVLVREDFEMECCSHLPYIEQGMWLABQFKQKALGLLQTSRQAE-VIAPA 1033
QY 453 KEVLYQQVD-----EMECSSQAAPYIEQAQVIAHOFKEKVLGLDNDQVVTTP---DKEI 504
Db 1034 VQTNWQKLETFWAKHWNFIISGLQYLAGLSTLP--NPALIASIMAFPTAAVTSPLITSQTL 1091
QY 505 LYE-----AFDEMECASKAALIEEGORMAEMLKSKIQGLLG----- 541
Db 1092 LFNILGGWVAQAAPGATAFVGAGLAGAAGISVGLGKVLIDILAGYGAGVAGALVAFK 1151
QY 542 -----ILRRHVGPGEAGVQWNNRLIAFASRN 568
Db 1152 IMSGEVPTEDLVNLLPALSPGALVVGVCVCAAILRRHVGPGEAGVQWNNRLIAFASRN 1211
QY 569 HVSPTHYVPS----- 578
Db 1212 HVSPTHYVPSDAAARVTAISSLTWTQLRLRHQWISSECTPCSGSWLRDIWDWICEV 1271
QY 579 ----- 578
Db 1272 LSDFTKWLKALMPQLPGIPFVSCQGYKGVWRVDMHETRCHCGABIGHVKNGTMRIV 1331
QY 579 ----- 578
Db 1332 GPRTCNMWSGTFPINAYTTGCTPLPAPNYTFALWRVSAEYVEIRQVPSPEFTELDQ 1391
QY 579 -RSRRA-----QALPVWAREDY----- 595
Db 1392 VRLHRFAPPCPELLREEVSRVGLHVPVGSQLPCEPEPDVAULTSMLTDPSSHITAEAG 1451
QY 596 -----NPP-----LVET---WKK----- 605
Db 1452 RRLARGSPSVASSASQSLPASKATCTANHDSFDAELIEANLLRMGMGNITRVESE 1511
QY 606 -----PDYEPVWHG-----RSSRFAQALPVWARPDPYNPLVETWKKPDYE 647
Db 1512 NKWILDSFDPLVAEDEEREISVPAILRKSRFAQALFVWARPDPYNPLVETWKKPDYE 1571
QY 648 PPVWHG 653
Db 1572 PPVWHG 1577
```

```
RESULT 9
AAP90164
ID AAP90164 standard; protein; 2261 AA.
XX
AC AAP90164;
XX
DT 25-MAR-2003 (revised)
DT 01-NOV-1989 (first entry)
XX
DE Peptide encoded by composite hepatitis C virus cDNA.
XX
KW Hepatitis C virus; clone 12f; clone 15e; probe; vaccine.
XX
OS Pan troglodytes.
XX
PN GB2212511-A.
XX
PD 26-JUL-1989.
XX
PF 18-NOV-1988; 88GB-00027024.
XX
PR 18-NOV-1987; 87US-00122714.
PR 30-DEC-1987; 87US-00139886.
PR 26-FEB-1988; 88US-00161072.
PR 26-OCT-1988; 88US-00263584.
XX
PA (CHIR ) CHIRON CORP.
XX
PI Houghton M, Choo QL, Kuo G;
XX
DR WPI; 1989-215054/30.
DR N-PSDB; AAN90331.
XX
PT Hepatitis C virus gene - used for prodn. of polynucleotide probes
PT polypeptide(s) and antibodies for diagnosis, prevention and treatment of
PT infection.
XX
PS Disclosure; Fig 32; 30pp; English.
XX
CC The sequence is the peptide encoded by the composite hepatitis C virus
CC (HCV) cDNA of AAN90331. The polypeptides are used to diagnose HCV-induced
CC NANBH, to raise antibodies for immunoassay or treatment, or to produce
CC vaccines. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 2261 AA;
Query Match 36.5%; Score 1624.5; DB 1; Length 2261;
Best Local Similarity 36.1%, Pred. No. 6.2e-107;
Matches 399; Conservative 26; Mismatches 80; Indels 601; Gaps 15;
QY 146 TDNSPPVVPVPSQFVAHLHAPTSGSKSTKVPAAAYAAQGYKVLNPNPSVAATLFGGAYMSK 205
Db 586 TDNSPPVVPVPSQFVAHLHAPTSGSKSTKVPAAAYAAQGYKVLNPNPSVAATLFGGAYMSK 645
QY 206 AHGIDPNIRTVRTITGSPITYSTYKFLADGGCGGAYDIIICDECHSTDATSILGIG 265
Db 646 AHGIDPNIRTVRTITGSPITYSTYKFLADGGCGGAYDIIICDECHSTDATSILGIG 705
QY 266 TVLDQAGTAGARLVLATATPGSVTVPHNPHEEVALSTTGEIPFYGKAIPLEVIKGGRH 325
Db 706 TVLDQAGTAGARLVLATATPGSVTVPHNPHEEVALSTTGEIPFYGKAIPLEVIKGGRH 765
QY 326 LIFCHSKKCCDELAALVALGINAVAYRGDLVSIVPTSGDVVVVATDALTMTGYTGFDS 385
Db 766 LIFCHSKKCCDELAALVALGINAVAYRGDLVSIVPTSGDVVVVATDALTMTGYTGFDS 825
QY 386 VIDCNTC----- 392
Db 826 VIDCNTCVTQTVDFSIDPTFTTITLPODAVSRTOQRGRTGRGKGIYRFVAPGERPSG 885
QY 393 ----- 392
```

```
Db 886 MFDSSVLCBCYDAGCAWVELTPAETTVRLRAYMNTPLGVQCQDHLFEWGVFTGLTHIDA 945
Qy 393 -----
Db 946 HFLSQTQSGENLPYLVAQATVCARAQPPSWDMQMKLIRLKTPLHGTPLLYRGA 1005
Qy 393 -----ACSG 396
Db 1006 VQNEITLTHPVTKIMTMSADLEVTSTWLVGVLAALAAAYCLSTGCVVIGRVLSG 1065
Qy 397 KPAIIPREVLYRREFDEMECSQHLPYIEQGMMLAEQFKQKALGL-----SRGKPAIVPD 452
Db 1066 KPAIIPREVLYRREFDEMECSQHLPYIEQGMMLAEQFKQKALGLQQTASQAE-VIAPA 1124
Qy 453 KEVLYQQYD-----EMECSSAAYIEQAQVIAHQFKVKGLIDNDQVVTPT--DKEI 504
Db 1125 VQTNWQKLEFWAKHMMNFISGIIQYLAGLSLPG--NPAIASLMAFTAATVSPITTSOTL 1182
Qy 505 LYE-----AFDEMEECASKAALIEGORMAELKSKIQGLLG-----541
Db 1183 LFNILGGVAAQAAPGAATAFVGAGLAGAALGSVGLGKVLIDILAGYGAGVAGALVAFK 1242
Qy 542 -----ILRRHVGPGEAGAVOMNRLIAFASGN 568
Db 1243 IMSGEVPTSDLVNLLPAILSPGALVGVWCAAILRRHVGPGEAGAVOMNRLIAFASGN 1302
Qy 569 HVSPTHVPS-----578
Db 1303 HVSPTHVPSDAAARVAILSSLTVTOLLRLHQWISSECTTPCSGSWLRDIDWICEV 1362
Qy 579 -----578
Db 1363 LSDFKTLWAKLMPQLPGIPFVSCORGKGYWVRVDGIMHTRCHGAEITGHVKNGTWRIV 1422
Qy 579 -----578
Db 1423 GPRTCRNWSGTFPINAYTTGCTPLPAPNTYTFALMRVSAEYVEIRQGVDFHYVTGMTT 1482
Qy 579 -----RSRFEA-----QALPVWARPD 594
Db 1483 DNLKPCQVPSPPEFTELDGVRLHRFAPCPKPLREEVSRVGLHEYPVGSQLPCEPEPD 1542
Qy 595 Y-----NPP-----LV 600
Db 1543 VAVLTSMLTDSHITAERAGRLARGSPSVASSASQSLKATCTANHSDPAELI 1602
Qy 601 ET---WKK-----PDYEPVPHG-----RSRRFAQALPV 627
Db 1603 EANLLWRQEMGNITRVESENKVVILDSFDPLVAEEDEREISVPAEILRKSRFAQALPV 1662
Qy 628 WARDYNPPLVETWKKPDYEPVPHG 653
Db 1663 WAREDPNPLVETWKKPDYEPVPHG 1688

RESULT 10
AAP92050
ID AAP92050 standard; protein; 2436 AA.
XX
AC AAP92050;
XX
DT 25-MAR-2003 (revised)
DT 02-MAR-1990 (first entry)
XX
DE Sequence encoded in the hepatitis C virus (HCV) cDNA inserts in clones K9
DE -1 through 156.
XX
KW Hepatitis C virus (HCV); non-A, non-B hepatitis (HANBH).
XX
OS Hepatitis C virus.
XX
FN EP318216-A.
XX
```

```
PD 31-MAY-1989.
XX
XX 18-NOV-1988; 88EP-00310922.
XX
PR 18-NOV-1987; 87US-00122714.
PR 30-DEC-1987; 87US-00139886.
PR 26-FEB-1988; 88US-00161072.
PR 06-MAY-1988; 88US-00191263.
PR 26-OCT-1988; 88US-00263584.
PR 14-NOV-1988; 88US-00271450.
XX
PA (CHIR ) CHIRON CORP.
PA (CHIR ) CHIRON CORP.
XX
PI Houghton M, Choo QL, Kuo G;
XX
DR WPI; 1989-159274/22.
DR N-PSDB; AAN92106.
XX
XX Purified hepatitis C virus - and associated nucleic acids and
XX polypeptide(s).
XX
PS Claim 13; Fig 47-1-47-8; 139pp; English.
XX
CC It is the sequence encoded in the open reading frame of hepatitis C virus
CC (HCV) cDNA inserts in clones K9-1 through 156. It is antigenic and could
CC be used in immunoassay reagents and vaccines and to generate antibodies
CC useful in diagnosis and passive immunotherapy for HCV infection/non-A,
CC non-B hepatitis. (Updated on 25-MAR-2003 to correct PR field.) (Updated
CC on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 2436 AA;

Query Match 36.5%; Score 1624.5; DB 1; Length 2436;
Best Local Similarity 36.1%; Pred. No. 6.9e-107;
Matches 399; Conservative 26; Mismatches 80; Indels 60; Gaps 15;

Qy 146 TDNSPPVVPQSFQVLAHLHAPTGSKSTKVPAAVAAQGYKVLNLPNSVAATLGFAYMSK 205
Db 761 TDNSPPVVPQSFQVLAHLHAPTGSKSTKVPAAVAAQGYKVLNLPNSVAATLGFAYMSK 820
Qy 206 AHGIDPNIRTVRTITGSPITYSTYTGKFLADGGSGGAYDIIICDECHSDATSIILGIG 265
Db 821 AHGIDPNIRTVRTITGSPITYSTYTGKFLADGGSGGAYDIIICDECHSDATSIILGIG 880
Qy 266 TVLDOAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIIPYKAIPLVKGGRH 325
Db 881 TVLDOAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIIPYKAIPLVKGGRH 940
Qy 326 LIFCHSKKKCDLAALKVALGINAVAYRGLDVSIVPTSGDVVVVATDALTMTGTDGDFS 385
Db 941 LIFCHSKKKCDLAALKVALGINAVAYRGLDVSIVPTSGDVVVVATDALTMTGTDGDFS 1000
Qy 386 VIDNCTC-----392
Db 1001 VIDNCTCVTQVDFSLDPTFTIETITLPQDAVSRTORRGTRGKPGIYRFVAPGERPSG 1060
Qy 393 -----392
Db 1061 MFDSSVLCBCYDAGCAWVELTPAETTVRLRAYMNTPLGVQCQDHLFEWGVFTGLTHIDA 1120
Qy 393 -----392
Db 1121 HFLSQTQSGENLPYLVAQATVCARAQPPSWDMQMKLIRLKTPLHGTPLLYRGA 1180
Qy 393 -----ACSG 396
Db 1181 VQNEITLTHPVTKIMTMSADLEVTSTWLVGVLAALAAAYCLSTGCVVIGRVLSG 1240
Qy 397 KPAIIPREVLYRREFDEMECSQHLPYIEQGMMLAEQFKQKALGL-----SRGKPAIVPD 452
Db 1241 KPAIIPREVLYRREFDEMECSQHLPYIEQGMMLAEQFKQKALGLQQTASQAE-VIAPA 1299
```

QY	453	KEVLYQYD-----EMECGQAAPYIEBQAQVIAHQFKEKVLGLINDQVVVTP---DKEI	504
Db	1300	VQTNWQKLETFWAKHWNFFISGIOYLAGLSTLPG--NPATASLMAFTAAVTSPLTTQSQT	1357
QY	505	LYE-----AFDEMERCASKAALIEEGQRMWAEMLKSKIQGLLG-----	541
Db	1358	LFNILGWVAAQLAAPGAATAFVAGLAGAAGISVGLGKVLIDILLAGYGAGVAGALVAFK	1417
QY	542	-----ILREHVGPGEAGVOMNRLLIATAFASRGN	568
Db	1418	IMSGEVPSTEDLVNLLPAILSPGALVVGVCAAALIREHVGPGEAGVOMNRLLIATAFASRGN	1477
QY	569	HVSPETHVPS-----	578
Db	1478	HVSPETHVPSDAAARVAILSSITVTQLLRRLHOWISSECTTPCSGWLRLDWDWICEV	1537
QY	579	-----	578
Db	1538	LSDFKTLWKAKLWLPQLPGIFPVSCQGYKGVRVDGIMHTRCHCGAEITGHVXNGTMRIV	1597
QY	579	-----	578
Db	1598	GPTRCRNWGSTPFINAYTTGCTPLPAPNVTALWVSAEYVVEVQGVDFHVAGMIT	1657
QY	579	-----RGRFA-----QALPVMWARPD	594
Db	1658	DNLKPCQCVSPSEFFTELGGVRLHRFAPPCKPLIREVSVFRVGLHEYPVGSQSLPCBPEPD	1717
QY	595	Y-----NPP-----LV	600
Db	1718	VAVLTSMLTDPDSHITAEAGRRIARGSPVSVASSASQSLAPSUKATCTANHDSPPAELI	1777
QY	601	ET---WKK-----PDYPPPVVHG-----RSSRFAQALPV	627
Db	1778	EANLLWQEMGNITRVESENKVVILDSFDPLVAEEDERELISVPAELILKSRFAQALPV	1837
QY	628	WARPDYNPLVETWKKPDYPPPVVHG	653
Db	1838	WARPDYNPLVETWKKPDYPPPVVHG	1863
RESULT 11			
AAP90288			
ID	AAP90288 standard; protein; 2436 AA.		
XX	AC	AAP90288;	
XX	DT	(revised)	
DT	19-JUL-2001	(revised)	
DT	01-NOV-1989	(first entry)	
XX	XX		
DE	Peptide encoded by composite hepatitis C cDNA.		
KW	Hepatitis C virus; clone 15e; clone k9-1; probe; vaccine.		
XX	Pan troglodytes.		
XX	OS		
PN	GB212511-A.		
PD	26-JUL-1989.		
XX	18-NOV-1988;	88GB-00027024.	
XX	18-NOV-1987;	87US-00122714.	
PR	30-DEC-1987;	87US-00139886.	
PR	26-FEB-1988;	88US-00161072.	
PR	26-OCT-1988;	88US-00263584.	
XX	(CHIR) CHIRON CORP.		
XX			
PI	Houghton M, Choo QL, Kuo G;		
XX			
DR	WFI; 1989-215054/30.		

Db 1538 LSPDKTWLAKALPQLPIPVSCQGYKGVWYVDGIMHTRCHOGAEITGHVKNGTMRIV 1597
QY 579 ----- 578
Db 1598 GPRTCRNWSGTFPINAYTTGCTPLPAPNYTFALMRVSAEYVEIRQVGFHYVTGTT 1657
QY 579 -----RSREA-----QALPVWARP 594
Db 1658 DNLKPCQVSPPEFTTLDGVRHLRFAPPCPKLLREEVSRVGLHYPVGSQLPCEP 1717
QY 595 Y-----NPP-----LV 600
Db 1718 VAVLTSMLTDPSSHITAEAGRLARGSPPSVASSASQLSAPSLKATCTANHSDPAELI 1777
QY 601 ET---WKK-----PDYEPVVHG-----RSRRAQALPV 627
Db 1778 EANLLWRQEMGNITRVESENKVVILDSFDPLVAEEDEREISVPAEILRKSRRAQALPV 1837
QY 628 WARDYNPPLVETWKKPDYEPVVHG 653
Db 1838 WAREDYNAPPLVETWKKPDYEPVVHG 1863

RESULT 12

AA18540
ID AAB18540 standard; protein; 2772 AA.

XX AC AAB18540;

XX DT 15-JAN-2001 (first entry)

XX DE Protein encoded by a cDNA compiled Hepatitis C virus cDNA clones.

XX KW Hepatitis C virus; HCV; antisense polynucleotide; polyprotein;
XX KW viral infectivity; viral replication.

XX OS Hepatitis C virus.

XX PN EP1034785-A2.

XX PD 13-SEP-2000.

XX PF 16-MAR-1990; 2000EP-00109602.

XX PR 17-MAR-1989; 89US-00325338.

XX PR 20-APR-1989; 89US-00341334.

XX PR 18-MAY-1989; 89US-00355002.

XX PR 16-MAR-1990; 90EP-00302866.

XX PA (CHIR) CHIRON CORP.

XX PI Houghton M, Choo Q, Kuo G;

XX WPI; 2000-566891/53.

XX DR N-PSDB; AAA75296.

XX PT Novel composition comprising a hepatitis C virus antisense polynucleotide
XX PT which is complementary to or corresponds to a sense strand of the virus
XX PT genome, and selectively hybridizes to it.

XX PS Example; Fig 16; 75pp; English.

XX CC The specification describes a pharmaceutical composition which comprises
XX CC a hepatitis C virus (HCV) antisense polynucleotide. The HCV is
XX CC characterized by a positive stranded RNA genome which has 40% homology at
XX CC the polypeptide level to a HCV polyprotein. The antisense polynucleotide
XX CC binds to cellular polynucleotides which enhance and/or are required for
XX CC viral infectivity, replicative ability or chronicity. The antisense
XX CC polynucleotides may also be designed to bind with high specificity, to be
XX CC of increased stability, to be stable and to have low toxicity. The
XX CC composition also comprises an agent which causes viral RNA to be
XX CC inactive. The composition is used for preventing HCV replication in a

CC system. The present sequence is encoded by a novel HCV cDNA sequence,
CC which is used in the course of the invention
XX
SQ Sequence 2772 AA;

Query Match 36.5%; Score 1624.5; DB 3; Length 2772;
Best Local Similarity 36.1%; Pred. No. 8.2e-107;
Matches 399; Conservative 26; Mismatches 80; Indels 601; Gaps 15;

QY 146 TDNSPPVQSFQVAHLHAPTSGSKTKYPAAYAAQGYKVLNPNPSVAATLGRGAYMSK 205
Db 1097 TDNSPPVQSFQVAHLHAPTSGSKTKYPAAYAAQGYKVLNPNPSVAATLGRGAYMSK 1156
QY 206 AHGIDPNIRGVRITTTGSPITYSTYCKFLADGCGSGAYDIIICDECHSDATSIILGIG 265
Db 1157 AHGIDPNIRGVRITTTGSPITYSTYCKFLADGCGSGAYDIIICDECHSDATSIILGIG 1216
QY 266 TVLDOAETAGARLVVLTATATPPGSVTVPHNPIEFVALSTTGEIPFYKAIPLVVIKGRH 325
Db 1217 TVLDOAETAGARLVVLTATATPPGSVTVPHNPIEFVALSTTGEIPFYKAIPLVVIKGRH 1276
QY 326 LIFCHSKKKCDELAALVALGINAVAYYRGDVSIVPTSGDVVVVATDALMTGTGDFDS 385
Db 1277 LIFCHSKKKCDELAALVALGINAVAYYRGDVSIVPTSGDVVVVATDALMTGTGDFDS 1336
QY 386 VIDCNTC----- 392
Db 1337 VIDCNTCVTQTVDFSLDPTTETITLPODAVSTQRRGRGKPGIYRFVAFGERPSG 1396
QY 393 ----- 392
Db 1397 MFDSSVLCECYDAGCANVELTPAETTVRLRAYMNTPGIPVQDHLFEWGFVFTGLTHIDA 1456
QY 393 ----- 392
Db 1457 HFLSQTQSGENLPYLVAQATVCARAQPPSPDWQMKLIRLKLPTLHGTPLLYRGA 1516
QY 393 -----ACSG 396
Db 1517 VQNEITLTHPVTKYIMTMSADLEVTSTWLVGVGLAALAAAYCLSTGCVVIVGRVLSG 1576
QY 397 KPAIIPDREVLVREFDEMECSQHLPTYEQMMLAEQFKQKALGI-----SRGKPAIVPD 452
Db 1577 KPAIIPDREVLVREFDEMECSQHLPTYEQMMLAEQFKQKALGILOQTASQAE-VIAPA 1635
QY 453 KEVLYQQVD-----EMECSQAAPYIEQAQVIAHQEKEKVLGLDNDQVVTP---DKEI 504
Db 1636 VQTNWQKLETFWAKHMNFISGIIQYLAGLSTLPG--NPAIASLVAFATAVTSPLTTSQTL 1693
QY 505 LYE-----AFDEMECSKAALTEEGQRMALSKSQGLG----- 541
Db 1694 LFNILGGWVAAQLAAPGAATAFVGAGLAGAIGSVGLKVLIDILAGYGAGVAGALVAFK 1753
QY 542 -----IIRRHVGEGAVQVMNELLIAFASGN 568
Db 1754 IMSGEVFPSTDLVNLPAILSPGALVGVVCAAILRRHVGPGEAVQVMNELLIAFASGN 1813
QY 569 HVSPTHVPS----- 578
Db 1814 HVSPTHVPSDAAARVAILSSLTVQLRLRHQWISSECTTFCSGSWLRDWDWICEV 1873
QY 579 ----- 578
Db 1874 LSDFKTLWAKLMPQLPIPVSCQGYKGVWYVDGIMHTRCHOGAEITGHVKNGTMRIV 1933
QY 579 ----- 578
Db 1934 GPRTCRNWSGTFPINAYTTGCTPLPAPNYTFALMRVSAEYVEIRQVGFHYVTGTT 1993
QY 579 -----RSRFA-----QALPVWARP 594
Db 1994 DNLKPCQVSPPEFTTLDGVRHLRFAPPCPKLLREEVSRVGLHYPVGSQLPCEP 2053

QY 595 Y-----NPP-----IV 600
: : :
Db 2054 VAVLTSMLTDPSHITAEAGRLARGSPPSVASSASQISAPSLKATCTCTANHSDPAELI 2113
601 ET---WKK-----PDYEPVVHG-----RSSRFAQALPV 627
2114 EANLLWRQMGNIIRVSESNKVVILSDPDLVABEDEREISVPAEILKSRFAQALPV 2173
QY 628 WARDYNPPLVETWKKPDYEPVVHG 653
2174 WARDYNPPLVETWKKPDYEPVVHG 2199
Db
RESULT 13
RAY14975
ID AAY14975 standard; protein; 2955 AA.
XX AC AAY14975;
XX
DT 20-MAR-2003 (revised)
DT 08-NOV-1999 (first entry)
XX
XX Amino acid sequence of HCV-1 ORF.
DE
XX Hepatitis C virus; HCV; J1; J7; HCV-1; non-A, non-B HCV; NANBH;
KW HCV infection; vaccine.
XX
OS Hepatitis C virus.
XX
XX Key Location/Qualifiers
FH Misc-difference 441
FT /note= "encoded by Tt"
FT Misc-difference 461
FT /note= "encoded by CCCC"
XX
XX EP939128-A2.
XX
XX 01-SEP-1999.
XX 17-SEP-1990; 99EP-00101746.
XX
XX 15-SEP-1989; 89US-00408045.
XX 21-DEC-1989; 89US-00456142.
XX 17-SEP-1990; 90EP-00310149.
XX
XX (OYAA/) OYA A.
XX (CHTR) CHIRON CORP.
XX
XX Miyamura T, Saito I, Houghton M, Weiner AJ, Han J, Kolberg JA;
XX Cha T, Irvine BD;
XX
XX WPI; 1999-480843/41.
XX N-PSDB; AAZ07656.
XX
XX New Hepatitis C Virus isolates, useful for diagnosis of hepatitis
XX infections and development of vaccines.
XX
XX Disclosure; Fig 12; 132pp; English.
XX
XX The invention provides two new isolates of hepatitis C virus (HCV), J1
XX and J7. These two isolates comprise nucleotide and amino acid sequences
XX that are distinct from the HCV isolate HCV-1. The nucleotide sequences
XX may be used to detect non-A, non-B HCV (NANBH) polynucleotides by
XX hybridisation for diagnosis of NANBH infections. They may also be used to
XX screen blood donors, donated blood and blood products for this infection.
XX The isolates may also be used to isolate other naturally occurring
XX variants of the virus. The polypeptides may be used as a vaccine for
XX administration to patients to protect against infection with NANBH. The
XX present sequence represents the amino acid sequence of HCV-1 ORF.
XX (Updated on 20-MAR-2003 to correct PF field.) (Updated on 20-MAR-2003 to
XX correct PR field.)
XX
XX Sequence 2955 AA;

Query Match 36.5%; Score 1624.5; DB 2; Length 2955;
Best Local Similarity 36.1%; Pred. No. 9e-107;
Matches 399; Conservative 26; Mismatches 80; Indels 601; Gaps 15;
QY 146 TDNSPPVPPVPSQVVAHLHAPTSGSKSTKPAAYAAQGVKVLNPSVAATLGFAYMSK 205
1211 TDNSPPVPPVPSQVVAHLHAPTSGSKSTKPAAYAAQGVKVLNPSVAATLGFAYMSK 1270
QY 206 AHGIDPNIRTGVRTITITGSPITYSTYKFLADGGCGGAYDIIICDECHSTDATSIILG 265
1271 AHGIDPNIRTGVRTITITGSPITYSTYKFLADGGCGGAYDIIICDECHSTDATSIILG 1330
QY 286 TVLDOAETAGARLVVLTATATPPGSVTVPHPNIEEVALSTTGTGPIFYKAIPLEVIKGRH 325
1331 TVLDOAETAGARLVVLTATATPPGSVTVPHPNIEEVALSTTGTGPIFYKAIPLEVIKGRH 1390
QY 326 LIFCHSKKKCDELAALKVALGINAVYRGLDVSVIPTSGDVVVVATDALMTGYTGDFDS 385
1391 LIFCHSKKKCDELAALKVALGINAVYRGLDVSVIPTSGDVVVVATDALMTGYTGDFDS 1450
QY 386 VIDCNTC----- 392
1451 VIDCNTCVTQVDFSLDPTFTTITLPODAVSRQTQRRGTGRGKPGIVRFVAPGERPSG 1510
QY 393 ----- 392
1511 MPDSSVLCEDYDAGCAWYELTPAETTVRLRAYMNTFGLPVCQDHLFEWGVTFGLTHIDA 1570
QY 393 ----- 392
1571 HFLSQTKSGENLPYLVAQATVCARAQAPPPSWDMKCLIRLKPTLHGPTPLLYRLGA 1630
QY 393 -----ACSG 396
1631 VQNEITLTHPVTKYIMTCSADLEVVTVTLVGGVLAALAAAYCLSTGCVWIVGRVWLSG 1690
QY 397 KPAAIPDREVLYRPFDEMEECSSQHLPYIEQGMMLAEQFKQKALGL-----SRGKPAIYPD 452
1691 KPAAIPDREVLYRPFDEMEECSSQHLPYIEQGMMLAEQFKQKALGLQATASRAE-VIAPA 1749
QY 453 KEVLYQQYD-----EMEECSQAAPYIEQAQVIAHQFKEKVLGLIDNDQVWVTP--DKEI 504
1750 VQTNMQKLETFWAKHWNPFISGIQYLAGLSTUPG--NPAIASLMAFTAAVTSPLTTSQTL 1807
QY 505 LYE-----AFDEMEECASKAALIEEQGMMAELKSKITQGLG----- 541
1808 LFNILGGWVAAQLAAPGAATAFVGAGLAGAAGISVGLGKVLIDILAGYGAGVAGALVAFK 1867
QY 542 -----ILRRHVGPGEAGVOWWNRLLIAFASRGN 568
1868 IMSGEVPESTDLVNLPAILSPGALVGVVCAAILRRHVGPGEAGVOWWNRLLIAFASRGN 1927
QY 569 HVSPHYVPS-----RSRFA-----QALPVWARDP 594
1928 HVSPHYVPSDAAARVTAILLSLVTQLRLRHOWISECTTPCSGSLRINDWICEV 1987
QY 579 ----- 578
1988 LSDFXTLWAKALMPQLPGIPFVSCQRYKGVWRVDGIMHTRCHCGAEITGHVKNGTMRIV 2047
QY 579 ----- 578
2048 GPRTCRNWMSGTFPINAIVTTGCTPLPAPNTYFALWRVSAEYVEIRQVGFHYVTGMTT 2107
QY 579 -----RSRFA-----QALPVWARDP 594
2108 DNLCFCQVPSPEPFTDGLVRLHFPAPCKPLLRBEVSFRVGLHEYPVGSQPCPEPDP 2167
QY 595 Y-----NPP-----IV 600
2168 VAVLTSMLTDPSHITAEAGRLARGSPPSVASSASQISAPSLKATCTCTANHSDPAELI 2227
Db

```
Qy 601 ET---WKK-----PDYEPVVHG-----RSSRFAQALPV 627
Db 2228 EANLWQEMGNITRVESKNVILDSFDPLVAEEDEREISVPAEILKRSRFAQALPV 2287
Qy 628 WARDYNPPLVETWKKDDYPPVVHG 653
Db 2288 WARDYNPPLVETWKKDDYPPVVHG 2313
```

RESULT 14

```
AA18541
ID AAB18541 standard; protein; 2955 AA.
```

```
XX AC
```

```
XX AAB18541;
```

```
XX DT 15-JAN-2001 (first entry)
```

```
XX DE Polypeptide encoded by sense strand of HCV.
```

```
XX KW Hepatitis C virus; HCV; antisense polynucleotide; polyprotein;
```

```
XX KW viral infectivity; viral replication.
```

```
XX OS Hepatitis C virus.
```

```
XX PN EP1034785-A2.
```

```
XX PD 13-SEP-2000.
```

```
XX PF 16-MAR-1990; 2000EP-00109602.
```

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XX PR 17-MAR-1989; 89US-00325338.
```

```
XX PR 20-APR-1989; 89US-00341334.
```

```
XX PR 18-MAY-1989; 89US-00355002.
```

```
XX PR 16-MAR-1990; 90EP-00302866.
```

```
XX PA (CHIR ) CHIRON CORP.
```

```
XX PI Houghton M, Choo Q, Kuo G;
```

```
XX DR WPI; 2000-566891/53.
```

```
XX DR N-PSDB; AAA75297.
```

```
XX Novel composition comprising a hepatitis C virus antisense polynucleotide
PT which is complementary to or corresponds to a sense strand of the virus
PT genome, and selectively hybridizes to it.
PT Example; Fig 17; 75pp; English.
```

```
XX The specification describes a pharmaceutical composition which comprises
CC a hepatitis C virus (HCV) antisense polynucleotide. The HCV is
CC characterized by a positive stranded RNA genome which has 40% homology at
CC the polypeptide level to a HCV polyprotein. The antisense polynucleotide
CC binds to cellular polynucleotides which enhance and/or are required for
CC viral infectivity, replicative ability or chronicity. The antisense
CC polynucleotides may also be designed to bind with high specificity, to be
CC of increased stability, to be stable and to have low toxicity. The
CC composition also comprises an agent which causes viral RNA to be
CC inactive. The composition is used for preventing HCV replication in a
CC system. The present sequence is encoded by a novel HCV cDNA sequence,
CC which is used in the course of the invention
```

```
XX SQ Sequence 2955 AA;
```

```
Query Match 36.5%; Score 1624.5; DB 3; Length 2955;
Best Local Similarity 36.1%; Pred. No. 9e-107;
Matches 399; Conservative 26; Mismatches 80; Indels 601; Gaps 15;
```

```
Qy 146 TDNSPPVPQSFQVAHLHAPTGSKSTKVPAAVAAQGYKVLNLPVVAATLGFAYMSK 205
```

```
Db 1211 TDNSPPVPQSFQVAHLHAPTGSKSTKVPAAVAAQGYKVLNLPVVAATLGFAYMSK 1270
```

```
Qy 206 AHGIDPNIRGVRTITGSPITYTGKFLADGCGSGAYDIILICDECHSDATSIILGIG 265
```

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|||||
```

```
Db 1271 AHGIDPNIRGVRTITGSPITYTGKFLADGCGSGAYDIILICDECHSDATSIILGIG 1330
Qy 266 TVLDOAETAGARLVLTATATPPGSVTVPHNIEVALSTTGEIPYKAIPLVYKGRH 325
|||||
Db 1331 TVLDOAETAGARLVLTATATPPGSVTVPHNIEVALSTTGEIPYKAIPLVYKGRH 1390
|||||
Qy 326 LIFCHSKKCKDELAALVALGINAVAYRGLDVSVIPTSGDVVVVATDALTMTGTGDFDS 385
|||||
Db 1391 LIFCHSKKCKDELAALVALGINAVAYRGLDVSVIPTSGDVVVVATDALTMTGTGDFDS 1450
|||||
Qy 386 VIDCNC----- 392
|||||
Db 1451 VIDCNCVTQTVDFSLDPTFTTITLTPQDAVSTQRRGTRGKPGIYRFVAPCERPSG 1510
|||||
Qy 393 ----- 392
Db 1511 MFDSSVLCEYDAGCAWVELTPAETTVRLRAYMNTPLGVCQDHLFEWFGVFTGLTHIDA 1570
|||||
Qy 393 ----- 392
Db 1571 HFLSQTKSGENLPYLVAQATVCARAQAPPSWDQXWKCLIRLKLPTLHGFTPLLYRLGA 1630
|||||
Qy 393 -----ACSG 396
|||||
Db 1631 VQNEITLTHPVTKYIMTMSADLEVVTSTWLVGGVLAALAAAYCLSTGCVVIVGRVVLGS 1690
|||||
Qy 397 KPAPIPREVLYREFDEMECSQHLPLYEQGMMLAEQFKOKALGI-----SRGKPAIVPD 452
|||||
Db 1691 KPAPIPREVLYREFDEMECSQHLPLYEQGMMLAEQFKOKALGI-----SRGKPAIVPD 1749
|||||
Qy 453 KEVLYQQYD-----EMEECSQAAPYIEQAQVIAHQFKEKVLGLIDNDQVVVTP---DKEI 504
|||||
Db 1750 VQTNWQKLETFWAKHWNFISGIQYLAGLSILPG--NPATASLWAFATAVTSPLTTSQTL 1807
|||||
Qy 505 LYE-----AFDEMECASKAALIEGQRMALMKSKIQGLLG----- 541
|||||
Db 1808 LFNILGGVAAQLAAPGAATAFVAGLAGAAGAAIGSGVLGLIDILAGYAGVAGALVAFK 1867
|||||
Qy 542 -----ILRRHVGPGEAGVQMMNRLIAPASRGN 568
|||||
Db 1868 IMSGEVSTEDLVNMLPAILSPGALVGVVCAALIRRHVGPGEAGVQMMNRLIAPASRGN 1927
|||||
Qy 569 HVSPTHYVPS----- 578
|||||
Db 1928 HVSPTHYVPSDAAARVTAIILSLVTQLRLRLHQWISSECTTFCSGSLRLDINDWICEV 1987
|||||
Qy 579 ----- 578
Db 1988 LSDFKTLWAKLMPQLGIPFVSCQGYKGVWRVYDGMHTRCHCGAEITGHVKNGTWRIV 2047
|||||
Qy 579 ----- 578
Db 2048 GPTRCNWMSGTFPINAYTTGCTPLPAPNYTFALWRVSAEYVEIRQVGFHYVTGMTT 2107
|||||
Qy 579 -----RGRFA-----QALPVWARP 594
|||||
Db 2108 DNLKCPQVPSBFFTELDGVLRLHFAPCPKPLIREVSRVGLHEYPVGSQLPCEPEPD 2167
|||||
Qy 595 Y-----NPP-----LV 600
|||||
Db 2168 VAVLTSMLTDPSSHITAEAGRLARLARGSPFSSVASSASQLSAPSLKATCTANHDSFDAL 2227
|||||
Qy 601 ET---WKK-----PDYEPVVHG-----RSSRFAQALPV 627
|||||
Db 2228 EANLWQEMGNITRVESKNVILDSFDPLVAEEDEREISVPAEILKRSRFAQALPV 2287
|||||
Qy 628 WARDYNPPLVETWKKDDYPPVVHG 653
|||||
Db 2288 WARDYNPPLVETWKKDDYPPVVHG 2313
|||||
```

```
RESULT 15
AAR21519
```


Db 1808 LFNILGGWAAQAAAPGAATAFVGAGLAGAAGSVGLKVLIDILAGYGAGVAGALVAFK 1867
QY 542 -----ILRRHVGPGEAVOMNELLIAFASRGN 568
Db 1868 IMSGEVSTEDLVNLLPAILSPGALVGVVCAAILRRHVGPGEAVOMNELLIAFASRGN 1927
QY 569 HVSPTHVPS-----578
Db 1928 HVSPTHVPSDAAARVTAILLSSLTVTQLLRHLHQWISSECTTFCSSGSLWLDWDWICEV 1987
QY 579 -----578
Db 1988 LSDFKTWLKAKLMPQLPGIPFVSCQGYGVVRVDGIMHTRCHGCAETGHVKNGTMRIV 2047
QY 579 -----578
Db 2048 GPRTCRNWMSGTFPPINAYTTGCTPLPAPNYTFALWVSAEYVEIROVGFHYVTGWT 2107
QY 579 -----RSTRFA-----QALPVWARP 594
Db 2108 DNLKPCQVPSPEFFTELDGVRHLHRFPCKPLREEVSRVGLHEYPVGSQLPCEPEPD 2167
QY 595 Y-----NPP-----LV 600
Db 2168 VAVLTSMLTDPSHITAEAGRRLARGSPSVASSASQLSAPSLKATCTANHDSFDAELI 2227
QY 601 ET---WKK-----PDYEPVYHG-----RSSRFAQALPV 627
Db 2228 EANLLRQEMGNGNTRVESENKVVILDSFDPLVAEEDREISVPABILKXSRFAQALPV 2287
QY 628 WARDYNPPLVETWKKPDYEPVYHG 653
Db 2288 WARDYNPPLVETWKKPDYEPVYHG 2313

Search completed: June 21, 2004, 10:30:18
Job time : 64.4736 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 21, 2004, 10:18:09 ; Search time 40.9396 Seconds

(without alignments)
4734.482 Million cell updates/sec

Title: US-10-658-782-2

Perfect score: 3619

Sequence: 1 MAPITAYAQTRGLGLCIIT.....PALIPDREVLRYFDEMEEC 686

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query %	Score	Match	Length	DB ID	Description
1	3619	100.0	686	5	AAU76377	Hepatitis
2	3619	100.0	686	5	AAE18689	HCV-1 NS3
3	3619	100.0	686	6	ABG72261	HCV-1 NS3
4	3619	100.0	686	7	ADC06767	HCV mutan
5	3602	99.5	2261	1	AAp90164	Peptide e
6	3602	99.5	2436	1	AAp92050	Sequence
7	3602	99.5	2436	1	AAp90288	Peptide e
8	3602	99.5	2772	3	AAAB18540	Protein e
9	3602	99.5	2955	2	AAV14975	Amino aci
10	3602	99.5	2955	3	AAAB18541	Polyprote
11	3602	99.5	3011	2	AAAR90931	Hepatitis
12	3602	99.5	3011	2	AAAW34480	HCV polyp
13	3602	99.5	3011	2	AAAW40038	HCV polyp
14	3602	99.5	3011	5	AAAE22049	Hepatitis
15	3600	99.5	728	5	AAE18688	NS3/4a mu
16	3600	99.5	728	7	ADC06766	HCV mutan
17	3599	99.4	2301	1	AAAP92047	Sequence
18	3595	99.3	2772	2	AAAR08123	Hepatitis
19	3594	99.3	686	4	AAAB62633	HCV NS3A
20	3593	99.3	3011	2	AAAR21519	Compiled
21	3590	99.2	2435	2	AAAR25135	HCV polyp
22	3589	99.2	3011	2	AAAR31621	Hepatitis
23	3587	99.1	3011	5	AAAU84597	HCV polyp
24	3586	99.1	2816	2	AAAR34009	HCV-1 pol
25	3583	99.0	1786	1	AAAP90158	Protein s

26	3583	99.0	2436	2	AAAR28582	AAr28582 HCV amino
27	3583	99.0	2894	2	AAAR70230	AAr70230 Composite
28	3580	98.9	2894	2	AAAR24440	AAr24440 Composite
29	3579	98.9	1766	1	AAp92041	AAp92041 Hepatitis
30	3565	98.5	686	5	AAE21837	AAe21837 Hepatitis
31	3565	98.5	686	5	AAE19900	AAe19900 Hepatitis
32	3565	98.5	686	7	ABW00351	ABw00351 Hepatitis
33	3561	98.4	686	5	AAE21838	AAe21838 Hepatitis
34	3561	98.4	686	5	AAE19907	AAe19907 Hepatitis
35	3561	98.4	686	7	ABW00358	ABw00358 Hepatitis
36	3561	98.4	3011	2	AAAR40120	AAr40120 HCV genom
37	3560	98.4	686	5	AAE21840	AAe21840 Hepatitis
38	3560	98.4	686	5	AAE19919	AAe19919 Hepatitis
39	3560	98.4	686	7	ABW00370	ABw00370 Hepatitis
40	3560	98.4	2955	2	AAAR08124	AAr08124 Hepatitis
41	3560	98.4	3011	2	AAAW77397	AAw77397 Hepatitis
42	3560	98.4	3011	6	ABP71460	ABp71460 Amino aci
43	3560	98.4	3012	5	AAU99289	AAu99289 Hepatitis
44	3560	98.4	3012	6	ABU61848	ABu61848 HCV H77 C
45	3559	98.3	686	5	AAE21843	AAe21843 Hepatitis

ALIGNMENTS

RESULT 1
AAU76377
ID AAU76377 standard; protein; 686 AA.
XX
AC AAU76377;
XX
DT 08-MAY-2002 (first entry)
XX
DE Hepatitis C virus NS3/4a conformational epitope protein sequence.
XX
KW Hepatitis C virus; HCV; NS3/4a conformational epitope; seroconversion;
KW immunoassay solid support; multiple epitope fusion antigen; MEFA;
KW non-structural protein; mutant; mutein.
XX
OS Hepatitis C virus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 403 /note= "Wild-type Thr substituted by Pro"
FT Misc-difference 404 /note= "Wild-type Ser substituted by Ile"
FT
FT
XX WO200196870-A2.
XX
XX 20-DEC-2001.
XX
XX 14-JUN-2001; 2001WO-US019156.
XX
XX 15-JUN-2000; 2000US-0212082P.
XX 02-APR-2001; 2001US-0280811P.
XX 02-APR-2001; 2001US-0280867P.
XX (CHIR) CHIRON CORP.
XX Chien DY, Arcangel P, Tandeske L, George-Nascimento C, Coit D;
XX Medina-Selby A;
XX WPI; 2002-090228/12.
XX N-PSDB; ABK15344.
XX
XX Immunoassay solid support, useful for detecting hepatitis C virus
XX infection in biological sample, comprises HCV NS3/4a conformational
XX epitope and multiple epitope fusion antigen bound to the support.
XX Claim 5; Fig 3; 92pp; English.
XX
XX The present invention relates to a new immunoassay solid support
CC

CC consisting essentially of at least one hepatitis C virus (HCV) NS3/4a
CC conformational epitope and a multiple epitope fusion antigen (MEFA),
CC bound to the support. The NS3/4a conformational epitope and/or MEFA
CC reacts specifically with anti-HCV antibodies present in a biological
CC sample from an HCV-infected individual. The immunoassay of the invention
CC is useful for detecting hepatitis C virus infection in a biological
CC sample. The method of the invention provides a sensitive, accurate
CC diagnostic and prognostic tool to provide adequate patient care and to
CC prevent transmission of HCV by blood and by blood products, or by
CC personal contact. Use of NS3/4a conformational epitope in combination
CC with MEFA, provides a sensitive and reliable method for detecting early
CC HCV seroconversion. Use of MEFA has the added advantages of decreasing
CC masking problems, improving sensitivity in detecting antibodies by
CC allowing a greater number of epitopes on a unit surface area of
CC substrate, and improving substrate. Detection accuracy is increased and
CC the incidence of false results is reduced because of the identification
CC and the use of highly immunogenic HCV antigens which are present during
CC the early stages of HCV seroconversion. The present amino acid sequence
CC represents the non-structural protein NS3/4a conformational epitope of
CC the invention
XX
SQ Sequence 686 AA;
Query Match 100.0%; Score 3619; DB 5; Length 686;
Best Local Similarity 100.0%; Pred. No. 1.6e-306;
Matches 686; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPITAYAAQTRGLGCIITSLTGRDNQVGEVQIVSTAAQTFLATCINGVCTVYHGA 60
DB 1 MAPITAYAAQTRGLGCIITSLTGRDNQVGEVQIVSTAAQTFLATCINGVCTVYHGA 60
QY 61 GTTITASPKGVQIOMYTNVDQDLVGPAPQSGRSITPTCTCGSSDLYLVTRHADVIPVRR 120
DB 61 GTTITASPKGVQIOMYTNVDQDLVGPAPQSGRSITPTCTCGSSDLYLVTRHADVIPVRR 120
QY 121 GDSRGSLLSPRPISYLVKSGSGPLLCPAGHAGVIFRAAVCTRGVAKAVDFIPVENLET 180
DB 121 GDSRGSLLSPRPISYLVKSGSGPLLCPAGHAGVIFRAAVCTRGVAKAVDFIPVENLET 180
QY 181 RSPVFTDSSPPVQSFQVAHLHAPTGSKSTKVPAAAYAAQGYKVLVLPNSVAATLFG 240
DB 181 RSPVFTDSSPPVQSFQVAHLHAPTGSKSTKVPAAAYAAQGYKVLVLPNSVAATLFG 240
QY 241 AYMSKAGIDNITGVRTITTSPTITVSTYKFLADGCGGGAYDIIICDECHSDATS 300
DB 241 AYMSKAGIDNITGVRTITTSPTITVSTYKFLADGCGGGAYDIIICDECHSDATS 300
QY 301 ILGIGTVLDQAEATAGARLVILATATPPGSVTVPHNIEEVALSTTGEIPFYGKAIPLEVI 360
DB 301 ILGIGTVLDQAEATAGARLVILATATPPGSVTVPHNIEEVALSTTGEIPFYGKAIPLEVI 360
QY 361 KGGRHLLIFCHSKKKDELAALKVALGINAVAYYRGLDVSVPPIGDDVVVATDMLTGYT 420
DB 361 KGGRHLLIFCHSKKKDELAALKVALGINAVAYYRGLDVSVPPIGDDVVVATDMLTGYT 420
QY 421 GDFDSVIDCNTVQTVDPSLDPTTITITLPODAVSRTQRRGTGRKPGIYRFVAPG 480
DB 421 GDFDSVIDCNTVQTVDPSLDPTTITITLPODAVSRTQRRGTGRKPGIYRFVAPG 480
QY 481 ERPSGMFDSVLCBECYDAGCAWYELTPAETTVLRAYNMTPLGVPQDHLFEWGVFTGL 540
DB 481 ERPSGMFDSVLCBECYDAGCAWYELTPAETTVLRAYNMTPLGVPQDHLFEWGVFTGL 540
QY 541 THIDAHFLSQTKSGENIPYLVAQATVCARAQAPPSPSDQWKKLIRKPTLHGPTPLL 600
DB 541 THIDAHFLSQTKSGENIPYLVAQATVCARAQAPPSPSDQWKKLIRKPTLHGPTPLL 600
QY 601 YRLGAVQNEIITLTHPVTKYIMTMSADLEVTSTWLVGGVLAALAAAYCLSTGCVVIYGR 660
DB 601 YRLGAVQNEIITLTHPVTKYIMTMSADLEVTSTWLVGGVLAALAAAYCLSTGCVVIYGR 660
QY 661 VVLGSKPAIIPDREVLYREFDEMEEC 686
DB 661 VVLGSKPAIIPDREVLYREFDEMEEC 686

DB 661 VVLGSKPAIIPDREVLYREFDEMEEC 686

RESULT 2

AAE18689
ID AAE18689 standard; protein; 686 AA.

XX AAE18689;
AC
XX
XX 17-MAY-2002 (first entry)

XX HCV-1 NS3/4a mutant conformational antigen.

XX Hepatitis C virus; NS3/4a antigen; HCV infection; mutant; mutein.

XX Hepatitis C virus type 1.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 403 /note= "Wild type Thr substituted with Pro"

FT Misc-difference 404 /note= "Wild type Ser substituted with Ile"

XX WC200196875-A2.

XX 20-DEC-2001.

XX 14-JUN-2001; 2001WO-US019369.

XX 15-JUN-2000; 2000US-0212082P.

XX 02-APR-2001; 2001US-0280811P.

XX 02-APR-2001; 2001US-0280867P.

XX (CHIR) CHIRON CORP.

XX Chien DY, Arcangel P, Tandeske L, George-Nascimento C, Coit D;

XX Medina-Selby A;

XX WPI; 2002-179522/23.

XX N-PSDB; AAD29795.

XX Immunoassay solid support useful for detecting hepatitis C virus infection in a biological sample, comprises at least one of HCV anti-core antibody and HCV NS3/4a epitope, bound to the support.

XX Example 2; Fig 4; 87pp; English.

XX The present invention relates to hepatitis C virus (HCV) core antigen and NS (nonstructural) 3/4a antibody combination assay that can detect both HCV antigens and antibodies present in a sample using a single solid matrix as well as immunoassay solid supports for use in the assay. The solid support is useful for detecting HCV infection in a biological sample. The present sequence is HCV-1 NS3/4a mutant conformational antigen. This sequence is used in the exemplification of the invention

XX Sequence 686 AA;

Query Match 100.0%; Score 3619; DB 5; Length 686;

Best Local Similarity 100.0%; Pred. No. 1.6e-306;

Matches 686; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPITAYAAQTRGLGCIITSLTGRDNQVGEVQIVSTAAQTFLATCINGVCTVYHGA 60

DB 1 MAPITAYAAQTRGLGCIITSLTGRDNQVGEVQIVSTAAQTFLATCINGVCTVYHGA 60

QY 61 GTTITASPKGVQIOMYTNVDQDLVGPAPQSGRSITPTCTCGSSDLYLVTRHADVIPVRR 120

DB 61 GTTITASPKGVQIOMYTNVDQDLVGPAPQSGRSITPTCTCGSSDLYLVTRHADVIPVRR 120

QY 121 GDSRGSLLSPRPISYLVKSGSGPLLCPAGHAGVIFRAAVCTRGVAKAVDFIPVENLET 180

DB 121 GDSRGSLLSPRPISYLVKSGSGPLLCPAGHAGVIFRAAVCTRGVAKAVDFIPVENLET 180

```

QY 181 RSPVFTDSSPPVPPQSFQVAHLHAPTSGSKSTKVPAAVAAQGYKVLVLPNSVAATLFG 240
Db 181 RSEVFTDSSPPVPPQSFQVAHLHAPTSGSKSTKVPAAVAAQGYKVLVLPNSVAATLFG 240
QY 241 AYMSKAHGIDPNIRTVRTITGSPITYSTYKFLADGGCGSGAYDIIICDECHSTDATS 300
Db 241 AYMSKAHGIDPNIRTVRTITGSPITYSTYKFLADGGCGSGAYDIIICDECHSTDATS 300
QY 301 ILGIGTVLQDAETAGARLVVLATATPPGSVTVPHNPNEEVALSTTGEIPFYGKAIPLEVI 360
Db 301 ILGIGTVLQDAETAGARLVVLATATPPGSVTVPHNPNEEVALSTTGEIPFYGKAIPLEVI 360
QY 361 KGRHLIFCHSKKCKDELAALKVALGINAVAYRGLDVSVPPIGVVVVATDALMTGYT 420
Db 361 KGRHLIFCHSKKCKDELAALKVALGINAVAYRGLDVSVPPIGVVVVATDALMTGYT 420
QY 421 GDFDSVIDCNTCTVQTVDFSLDPTFTIETITLPQDAVSRTOGRGTRGKPGIYRFVAPG 480
Db 421 GDFDSVIDCNTCTVQTVDFSLDPTFTIETITLPQDAVSRTOGRGTRGKPGIYRFVAPG 480
QY 481 ERPSGMFDSVLCEDYDAGCAYELTPAETTVRLRAYMNTPLGVQDHLFEWEGVFTGL 540
Db 481 ERPSGMFDSVLCEDYDAGCAYELTPAETTVRLRAYMNTPLGVQDHLFEWEGVFTGL 540
QY 541 THIDAHFLSQTQSGENLYIAYQATVCARAQAPPPSDQWKKLIRLKLPTLHGPTPLL 600
Db 541 THIDAHFLSQTQSGENLYIAYQATVCARAQAPPPSDQWKKLIRLKLPTLHGPTPLL 600
QY 601 YRLGAVQNEITLTHPVTKYIMTCSADLEVVSTWLVGVGLAALAAAYCLSTGCVVIVGR 660
Db 601 YRLGAVQNEITLTHPVTKYIMTCSADLEVVSTWLVGVGLAALAAAYCLSTGCVVIVGR 660
QY 661 VVLGSKPALIPDREVLRYREFDEMEEC 686
Db 661 VVLGSKPALIPDREVLRYREFDEMEEC 686

RESULT 3
ID ABG72261 standard; protein; 686 AA.
AC ABG72261;
DT 06-MAR-2003 (first entry)
XX HCV-1 NS3/4a conformational antigen.
XX Immunassay solid support; Hepatitis C Virus type-1; HCV-1;
XX NS3/4a conformational epitope; multiple epitope fusion antigen; MEFA;
XX anti-HCV antibody; NS3/4a conformational antigen; HCV infection; mutant;
XX mutcin.
XX Hepatitis C virus type 1.
XX Synthetic.
FH Key Location/Qualifiers
FT Region
FT 2..686
FT /note= "Corresponds to amino acid residues 1027-1711 of
FT HCV-1 NS3/4a polypeptide"
FT Misc-difference 403
FT /note= "Substitution of wild-type Thr to Pro"
FT Misc-difference 404
FT /note= "Substitution of wild-type Ser to Ile"
XX US2002146685-A1.
XX 10-OCT-2002.
XX 14-JUN-2001; 2001US-00891654.
XX 15-JUN-2000; 2000US-0212082P.
XX 02-APR-2001; 2001US-0280811P.

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PR 02-APR-2001; 2001US-0280867P.
XX (CHIE/) CHIEN D Y.
PA (ARCA/) ARCANGEL P.
PA (TAND/) TANDESKE L.
PA (GEOR/) GEORGE-NASCIMENTO C.
PA (COIT/) COIT D.
XX (MEDI/) MEDINA-SELBY A.
PI Chien DY, Arcangel P, Tandeske L, George-Nascimento C, Coit D;
PI Medina-Selby A;
XX WPI; 2003-147573/14.
DR N-PSDB; ABX14410.
XX Immunassay solid support for detecting Hepatitis C Virus infection in
PT biological samples, comprises Hepatitis C Virus conformational epitope
PT and multiple epitope fusion antigen.
XX Claim 2; Fig 3A-3D; 45pp; English.
XX The present invention relates to immunoassays comprising Hepatitis C
CC Virus (HCV) NS3/4a conformational epitope and multiple epitope fusion
CC antigen (MEFA), bound to a solid support. The NS3/4a epitope and/or the
CC multiple epitope fusion antigen react with anti-HCV antibodies present in
CC a biological sample from an HCV-infected individual. The immunoassays and
CC methods of the invention are useful for detecting HCV infection in a
CC biological sample. The inventive immunoassay solid support provides a
CC sensitive and reliable method for detecting early HCV seroconversion. The
CC assays can detect HCV infection caused by any six known genotypes of HCV.
CC The use of the multiple epitope fusion proteins decreases masking
CC problems, improves sensitivity in detecting antibodies by allowing a
CC greater number of epitopes on a unit area of substrate, and improves
CC selectivity. The present sequence represents HCV type 1 (HCV-1) NS3/4a
CC conformational antigen, a mutant of the HCV-1 NS3/4a polypeptide
XX Sequence 686 AA;
SQ
Query Match 100.0%; Score 3619; DB 6; Length 686;
Best Local Similarity 100.0%; Pred. No. 1.6e-306;
Matches 686; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPITAYAAQOTRGLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVHGA 60
Db 1 MAPITAYAAQOTRGLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVHGA 60
QY 61 GTRTIASPKGPVIQMYTNVDQDLVGPAPQSGRSITPCTCGSSDLYLVTRHADVIPVRR 120
Db 61 GTRTIASPKGPVIQMYTNVDQDLVGPAPQSGRSITPCTCGSSDLYLVTRHADVIPVRR 120
QY 121 GDSRGLSPRPISYLVKSGSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTM 180
Db 121 GDSRGLSPRPISYLVKSGSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTM 180
QY 181 RSPVFTDSSPPVPPQSFQVAHLHAPTSGSKTKVPAAYAAQGYKVLVLPNSVAATLFG 240
Db 181 RSPVFTDSSPPVPPQSFQVAHLHAPTSGSKTKVPAAYAAQGYKVLVLPNSVAATLFG 240
QY 241 AYMSKAHGIDPNIRTVRTITGSPITYSTYKFLADGGCGSGAYDIIICDECHSTDATS 300
Db 241 AYMSKAHGIDPNIRTVRTITGSPITYSTYKFLADGGCGSGAYDIIICDECHSTDATS 300
QY 301 ILGIGTVLQDAETAGARLVVLATATPPGSVTVPHNPNEEVALSTTGEIPFYGKAIPLEVI 360
Db 301 ILGIGTVLQDAETAGARLVVLATATPPGSVTVPHNPNEEVALSTTGEIPFYGKAIPLEVI 360
QY 361 KGRHLIFCHSKKCKDELAALKVALGINAVAYRGLDVSVPPIGVVVVATDALMTGYT 420
Db 361 KGRHLIFCHSKKCKDELAALKVALGINAVAYRGLDVSVPPIGVVVVATDALMTGYT 420
QY 421 GDFDSVIDCNTCTVQTVDFSLDPTFTIETITLPQDAVSRTOGRGTRGKPGIYRFVAPG 480
Db 421 GDFDSVIDCNTCTVQTVDFSLDPTFTIETITLPQDAVSRTOGRGTRGKPGIYRFVAPG 480

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RESULT 8
AA18540
ID AAB18540 standard; protein; 2772 AA.
XX
AC AAB18540;
XX
DT 15-JAN-2001 (first entry)
XX
DE Protein encoded by a cDNA compiled Hepatitis C virus cDNA clones.
XX
KW Hepatitis C virus; HCV; antisense polynucleotide; polyprotein;
XX
KW viral infectivity; viral replication.
XX
OS Hepatitis C virus.
XX
PN EP1034785-A2.
XX
PD 13-SEP-2000.
XX
PF 16-MAR-1990; 2000EP-00109602.
XX
PR 17-MAR-1989; 89US-00325338.
XX
PR 20-APR-1989; 89US-00341334.
XX
PR 18-MAY-1989; 89US-00355002.
XX
PR 16-MAR-1990; 90EP-00302866.
XX
FA (CHIR) CHIRON CORP.
XX
PI Houghton M, Choo Q, Kuo G;
XX
DR WPI; 2000-566891/53.
XX
N-PSDB; AAA75296.

Novel composition comprising a hepatitis C virus antisense polynucleotide which is complementary to or corresponds to a sense strand of the virus genome, and selectively hybridizes to it.
Example; Fig 16; 75pp; English.

The specification describes a pharmaceutical composition which comprises a hepatitis C virus (HCV) antisense polynucleotide. The HCV is characterized by a positive stranded RNA genome which has 40% homology at the polypeptide level to a HCV polypeptide. The antisense polynucleotide binds to cellular polynucleotides which enhance and/or are required for viral infectivity, replicative ability or chronicity. The antisense polynucleotides may also be designed to bind with high specificity, to be of increased stability, to be stable and to have low toxicity. The composition also comprises an agent which causes viral RNA to be inactive. The composition is used for preventing HCV replication in a system. The present sequence is encoded by a novel HCV cDNA sequence, which is used in the course of the invention

Query Match 99.5%; Score 3602; DB 3; Length 2772;
Best Local Similarity 99.6%; Pred. No. 3.8e-304;
Matches 683; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

1 MAPITAYAAQQTGRLGCIITSITGRDKNOVEGEVQIVSTAAQTFLATCINGCVTVYHGA 60
912 LAPITAYAAQQTGRLGCIITSITGRDKNOVEGEVQIVSTAAQTFLATCINGCVTVYHGA 971
61 GTRTIASPKGPVIMYTNVDQDLVGNWPAQPSRSLTPTCTGSSDLYLVTRHADVIPVRR 120
972 GTRTIASPKGPVIMYTNVDQDLVGNWPAQPSRSLTPTCTGSSDLYLVTRHADVIPVRR 1031
121 GDSRGLSPRPISVLKSSGGLPLCPAGHAGVIFRAAVCTRGVAKAVDFIPVENLETM 180
1032 GDSRGLSPRPISVLKSSGGLPLCPAGHAGVIFRAAVCTRGVAKAVDFIPVENLETM 1091
181 RSPVFTDNSSPPVFPQSFQVAHLHAPTGGKSTKVPAAAYAGYKVLVLPNSVAATLGF 240
1092 RSPVFTDNSSPPVFPQSFQVAHLHAPTGGKSTKVPAAAYAGYKVLVLPNSVAATLGF 1151

QY 241 AYMSKAHGIDENIRTVRTITTTGSPITYTYGKFLADGCGSGGAYDIIICDECHSTDATS 300
Db 1152 AYMSKAHGIDENIRTVRTITTTGSPITYTYGKFLADGCGSGGAYDIIICDECHSTDATS 1211
QY 301 ILGIGTVLDQAEATAGARLVVLTATPPGCVTVPHNIEEVALSTTGEIFFYKKAIPLEVI 360
Db 1212 ILGIGTVLDQAEATAGARLVVLTATPPGCVTVPHNIEEVALSTTGEIFFYKKAIPLEVI 1271
QY 361 KXGRHLIFCHSKKKCDELAALVALGINAVAYYRGLDVSVPPIGDVVVATDALMTGYT 420
Db 1272 KXGRHLIFCHSKKKCDELAALVALGINAVAYYRGLDVSVPITSGDVVVVATDALMTGYT 1331
QY 421 GDFSDVIDCNTCVTQTVDFSLDPTFTTETITLPODAVSKTQRRGTGRGKPIYRFVAPG 480
Db 1332 GDFSDVIDCNTCVTQTVDFSLDPTFTTETITLPODAVSKTQRRGTGRGKPIYRFVAPG 1391
QY 481 ERPSGMFDSVLCRCYDAGCAWYELTPAETTVRLRAYNNTPLPVCODHLEFWEGVFTGL 540
Db 1392 ERPSGMFDSVLCRCYDAGCAWYELTPAETTVRLRAYNNTPLPVCODHLEFWEGVFTGL 1451
QY 541 THIDAHFLSQTKSGENLPYLVAQATVCARAQAPPPSWDQWKKLIKPLTHGPTLL 600
Db 1452 THIDAHFLSQTKSGENLPYLVAQATVCARAQAPPPSWDQWKKLIKPLTHGPTLL 1511
QY 601 YRLGAVQNEITLTHPVTKYIMTMSADLEVTSTWLVGGVLAALAAAYCLSTGCVVIVGR 660
Db 1512 YRLGAVQNEITLTHPVTKYIMTMSADLEVTSTWLVGGVLAALAAAYCLSTGCVVIVGR 1571
QY 661 VVLSGKPAIIPDREVLYRPFDEMEEC 686
Db 1572 VVLSGKPAIIPDREVLYRPFDEMEEC 1597

RESULT 9
AA14975
ID AAY14975 standard; protein; 2955 AA.
XX
AC AAY14975;
XX
DT 20-MAR-2003 (revised)
DT 08-NOV-1999 (first entry)
XX
DE Amino acid sequence of HCV-1 ORF.
XX
KW Hepatitis C virus; HCV; J1; J7; HCV-1; non-A, non-B HCV; NANBH;
KW HCV infection; vaccine.
XX
OS Hepatitis C virus.
XX
FH Key Location/Qualifiers
FT Misc-difference 441 /note= "encoded by TT"
FT Misc-difference 461 /note= "encoded by CCCC"
XX
PN EP939128-A2.
XX
PD 01-SEP-1999.
XX
PF 17-SEP-1990; 99EP-00101746.
XX
PR 15-SEP-1989; 89US-00408045.
PR 21-DEC-1989; 89US-00456142.
PR 17-SEP-1990; 90EP-00310149.
XX
FA (OYAA/) OYA A.
FA (CHIR) CHIRON CORP.
XX
PI Miyamura T, Saito I, Houghton M, Weiner AJ, Han J, Kolberg JA;
PI Cha T, Irvine BD;
XX
DR WPI; 1999-480843/41.

DR N-PSDB; AAZ07656.
XX New Hepatitis C Virus isolates, useful for diagnosis of hepatitis
PT infections and development of vaccines.
XX Disclosure; Fig 12; 132pp; English.
XX The invention provides two new isolates of hepatitis C virus (HCV), J1
CC and J7. These two isolates comprise nucleotide and amino acid sequences
CC that are distinct from the HCV isolate HCV-1. The nucleotide sequences
CC may be used to detect non-A, non-B HCV (NANBH) polynucleotides by
CC hybridisation for diagnosis of NANBH infections. They may also be used to
CC screen blood donors, donated blood and blood products for this infection.
CC The isolates may also be used to isolate other naturally occurring
CC variants of the virus. The polypeptides may be used as a vaccine for
CC administration to patients to protect against infection with NANBH. The
CC present sequence represents the amino acid sequence of HCV-1 ORF.
CC (Updated on 20-MAR-2003 to correct PF field.) (Updated on 20-MAR-2003 to
CC correct PR field.)
XX Sequence 2955 AA;
SQ

Query Match 99.5%; Score 3602; DB 2; Length 2955;
Best Local Similarity 99.6%; Pred. No. 4.2e-304;
Matches 683; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAPITAAQOTRGLGCIITSLTGRDNQVGEVQIVSTAAQTFLATCINGVCWTVVHGA 60
Db :|||||
QY 1026 LAPITAAQOTRGLGCIITSLTGRDNQVGEVQIVSTAAQTFLATCINGVCWTVVHGA 1085
Db :|||||
QY 61 GTRTIASPKGPVQMYTNVDQDLVGPAPQGSRLTPTCTCGSSDLYLVTTHADVIPVRRR 120
Db :|||||
QY 1086 GTRTIASPKGPVQMYTNVDQDLVGPAPQGSRLTPTCTCGSSDLYLVTTHADVIPVRRR 1145
Db :|||||
QY 121 GDSRGSLLSPRISYLYKSGSGGGLLCPAGHAGVIFRAAIVCTRGVAKAVDFIPVENLETTM 180
Db :|||||
QY 1146 GDSRGSLLSPRISYLYKSGSGGGLLCPAGHAGVIFRAAIVCTRGVAKAVDFIPVENLETTM 1205
Db :|||||
QY 181 RSPVFTDSSPPVVPQSFQVAHLHAPTGSKSTKVPAAAYAAQGYKVLVLPSPVAATLGF 240
Db :|||||
QY 1206 RSPVFTDSSPPVVPQSFQVAHLHAPTGSKSTKVPAAAYAAQGYKVLVLPSPVAATLGF 1265
Db :|||||
QY 241 AYMSKAHGIDPNRTGRTITTSPTIYTYGKFLADGCGSGGAYDIIICDECHSTDATS 300
Db :|||||
QY 1266 AYMSKAHGIDPNRTGRTITTSPTIYTYGKFLADGCGSGGAYDIIICDECHSTDATS 1325
Db :|||||
QY 301 ILGIGTVLDOAETAGARLVLAATPPGCVTVPHNPTEEVALSTTGIPYKGAIPLEVI 360
Db :|||||
QY 1326 ILGIGTVLDOAETAGARLVLAATPPGCVTVPHNPTEEVALSTTGIPYKGAIPLEVI 1385
Db :|||||
QY 361 KGRHLIFCHSKKCDLAKLVALGINAVAYRGLDVSVIPIPGDVVVVATDALMTGYT 420
Db :|||||
QY 1386 KGRHLIFCHSKKCDLAKLVALGINAVAYRGLDVSVIPIPGDVVVVATDALMTGYT 1445
Db :|||||
QY 421 GDFDSVIDCNTCVTQTVDLDFPTTETITLPQDAVSRTQRRGRTGKPGIYRFVAPG 480
Db :|||||
QY 1446 GDFDSVIDCNTCVTQTVDLDFPTTETITLPQDAVSRTQRRGRTGKPGIYRFVAPG 1505
Db :|||||
QY 481 ERPSGMFDSVLCBICYDAGCAWYELTFAETTVLRAYMTFGLPVCODHLEFWEQVETGL 540
Db :|||||
QY 1506 ERPSGMFDSVLCBICYDAGCAWYELTFAETTVLRAYMTFGLPVCODHLEFWEQVETGL 1565
Db :|||||
QY 541 THIDAHFSLQTKSGENLPYLVAQVACARAQAPPSWDQMKCLIRLKPTELHGPTPLL 600
Db :|||||
QY 1566 THIDAHFSLQTKSGENLPYLVAQVACARAQAPPSWDQMKCLIRLKPTELHGPTPLL 1625
Db :|||||
QY 601 YRLGAVONEITLTHPVTKYIMTCMSADLEVTSTWLVGGVLAALAAAYCISTGCWVIYGR 660
Db :|||||
QY 1626 YRLGAVONEITLTHPVTKYIMTCMSADLEVTSTWLVGGVLAALAAAYCISTGCWVIYGR 1685
Db :|||||
QY 661 VVLGSKPAITPDREVLYRBEFDEMEEC 686
Db :|||||
QY 1686 VVLGSKPAITPDREVLYRBEFDEMEEC 1711
Db :|||||

RESULT 10
AAB18541
ID AAB18541 standard; protein; 2955 AA.
XX AC AAB18541;
XX 15-JAN-2001 (first entry)
DT Polypeptide encoded by sense strand of HCV.
DE Hepatitis C virus; HCV; antisense polynucleotide; polyprotein;
XX viral infectivity; viral replication.
KW Hepatitis C virus.
OS Hepatitis C virus.
XX EF1034785-A2.
XX 13-SEP-2000.
XX 16-MAR-1990; 2000EP-00109602.
XX 17-MAR-1989; 89US-00325338.
PR 20-APR-1989; 89US-00341334.
PR 18-MAY-1989; 89US-00355002.
PR 16-MAR-1990; 90EP-00302866.
XX (CHIR) CHIRON CORP.
XX Houghton M, Choo Q, Kuo G;
XX WPI; 2000-556891/53.
DR N-PSDB; AAA75297.
XX Novel composition comprising a hepatitis C virus antisense polynucleotide
PT which is complementary to or corresponds to a sense strand of the virus
PT genome, and selectively hybridizes to it.
XX Example; Fig 17; 75pp; English.
XX The specification describes a pharmaceutical composition which comprises
CC a hepatitis C virus (HCV) antisense polynucleotide. The HCV is
CC characterized by a positive stranded RNA genome which has 40% homology at
CC the polypeptide level to a HCV polyprotein. The antisense polynucleotide
CC binds to cellular polynucleotides which enhance and/or are required for
CC viral infectivity, replicative ability or chronicity. The antisense
CC polynucleotides may also be designed to bind with high specificity, to be
CC of increased stability, to be stable and to have low toxicity. The
CC composition also comprises an agent which causes viral RNA to be
CC inactive. The composition is used for preventing HCV replication in a
CC system. The present sequence is encoded by a novel HCV cDNA sequence,
CC which is used in the course of the invention
XX Sequence 2955 AA;
SQ

Query Match 99.5%; Score 3602; DB 3; Length 2955;
Best Local Similarity 99.6%; Pred. No. 4.2e-304;
Matches 683; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAPITAAQOTRGLGCIITSLTGRDNQVGEVQIVSTAAQTFLATCINGVCWTVVHGA 60
Db :|||||
QY 1026 LAPITAAQOTRGLGCIITSLTGRDNQVGEVQIVSTAAQTFLATCINGVCWTVVHGA 1085
Db :|||||
QY 61 GTRTIASPKGPVQMYTNVDQDLVGPAPQGSRLTPTCTCGSSDLYLVTTHADVIPVRRR 120
Db :|||||
QY 1086 GTRTIASPKGPVQMYTNVDQDLVGPAPQGSRLTPTCTCGSSDLYLVTTHADVIPVRRR 1145
Db :|||||
QY 121 GDSRGSLLSPRISYLYKSGSGGGLLCPAGHAGVIFRAAIVCTRGVAKAVDFIPVENLETTM 180
Db :|||||
QY 1146 GDSRGSLLSPRISYLYKSGSGGGLLCPAGHAGVIFRAAIVCTRGVAKAVDFIPVENLETTM 1205
Db :|||||
QY 181 RSPVFTDSSPPVVPQSFQVAHLHAPTGSKSTKVPAAAYAAQGYKVLVLPSPVAATLGF 240
Db :|||||

Db	1206	RSPVFTDNSSPPVPSQSFQVAHLHAPTSGSKSTKVPAAAYAGYKVLVLPNSVAATLFG	1265
QY	241	AYMSKAHGIDPNIRGTGVRTITGSPITYSTYKFLADGGCGSGAYDIIICDCHSTDATS	300
Db	1266	AYMSKAHGIDPNIRGTGVRTITGSPITYSTYKFLADGGCGSGAYDIIICDCHSTDATS	1325
QY	301	ILGIGTVLDQAEATAGARLVVLATATPPGSVTVPHNIEEVALSTTGEIPFYKAIPLFVI	360
Db	1326	ILGIGTVLDQAEATAGARLVVLATATPPGSVTVPHNIEEVALSTTGEIPFYKAIPLFVI	1385
QY	361	KGRHLIFCHSKKKCDELAALKI VALGINAVAYYRGDLVSVPPIGDVVVATDALMTGYT	420
Db	1386	KGRHLIFCHSKKKCDELAALKI VALGINAVAYYRGDLVSVPPIGDVVVATDALMTGYT	1445
QY	421	GDVDSVIDCNTCVTQTVDFSLDPTFTTETITL PQDAVSRTOGRGKPGIYRFVAPG	480
Db	1446	GDVDSVIDCNTCVTQTVDFSLDPTFTTETITL PQDAVSRTOGRGKPGIYRFVAPG	1505
QY	481	ERPSGMFSSVLCCEYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLFEWEGVFTGL	540
Db	1506	ERPSGMFSSVLCCEYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLFEWEGVFTGL	1565
QY	541	THIDAHFLSOTKQSGENLPYLVAQATVCARAQAPPPSWDQWKCLIRLKP TLHGPTPL	600
Db	1566	THIDAHFLSOTKQSGENLPYLVAQATVCARAQAPPPSWDQWKCLIRLKP TLHGPTPL	1625
QY	601	YRLGAVQNEITLTHPVTYKIIMTCSADLEVVSTWVLVGGVLAALAAAYCLSTGCVVIVGR	660
Db	1626	YRLGAVQNEITLTHPVTYKIIMTCSADLEVVSTWVLVGGVLAALAAAYCLSTGCVVIVGR	1685
QY	661	VVLGSKPALIPDREVLYREFDEMEEC	686
Db	1686	VVLGSKPALIPDREVLYREFDEMEEC	1711
RESULT 11			
ID	AAR90931 standard; protein; 3011 AA.		
AC	AAR90931;		
XX			
XX			
DT	25-MAR-2003 (revised)		
DT	15-MAY-1996 (first entry)		
DE	Hepatitis C virus polyprotein.		
XX			
XX			
KW	Non-A non-B hepatitis virus; NANBH; HCV; antigen; detection; diagnosis;		
OS	Hepatitis C virus.		
XX			
Key	Location/Qualifiers		
FT	Misc-difference 1..122		
FT	/label= antigen		
FT	/note= "C22; AAR90936"		
FT	Misc-difference 199..328		
FT	/label= antigen		
FT	/note= "S2; AAR90935"		
FT	Misc-difference 1192..1457		
FT	/label= antigen		
FT	/note= "C33c; AAR90932"		
FT	Misc-difference 1569..1931		
FT	/label= antigen		
FT	/note= "C100; AAR90933"		
FT	Misc-difference 2054..2464		
FT	/label= antigen		
FT	/note= "NS5; AAR90934"		
XX			
PN	EP693687-A1.		
XX			
PD	24-JAN-1996.		
XX			

PF	03-APR-1991;	95EP-00114016.	
XX			
PR	04-APR-1990;	90US-00504352.	
XX			
PA	(CHIR)	CHIRON CORP.	
XX			
PI	Houghton M, Choo Q, Kuo G;		
XX			
DR	WPI; 1996-117956/13.		
DR	N-PSDB; AAT12710.		
XX			
PT	Combinations of synthetic Hepatitis C Virus antigens - provide more effective diagnosis of Non-A, Non-B Hepatitis.		
XX			
PS	Disclosure; Fig 1(A-Y); 53pp; English.		
XX			
CC	The combination comprises an HCV antigen from the C domain (pref. C22 - AAR90936) and at least one HCV antigen from the NS3 (pref. C33c - AAR90933), NS4 (pref. C100 - AAR90933), S (pref. S2 - AAR90935) or NS5 (AAR90934) domain. The antigens may in the form of a fusion protein, a simple physical mixture, or the individual antigens commonly bound to a solid matrix. They are pref. prepd. by recombinant DNA techniques (primers are given in AAT12711-12716), but can be synthesised or isolated from HCV using affinity chromatography. (Updated on 25-MAR-2003 to correct PF field.)		
XX			
SQ	Sequence 3011 AA;		
	Query Match	99.5%; Score 3602; DB 2; Length 3011;	
	Best Local Similarity	99.6%; Pred. No. 4.3e-304;	
	Matches 683; Conservative	1; Mismatches 2; Indels 0; Gaps 0;	
QY	1	MAPITAYAAQOTRGLGCIITSITGRDKNQVEGEVQIVSTAAQTFLATCINGVCMTVYHGA	60
Db	1026	LAPITAYAAQOTRGLGCIITSITGRDKNQVEGEVQIVSTAAQTFLATCINGVCMTVYHGA	1085
QY	61	GTRTIASPKGPVIQWYTNVDQLVGNPAPQGSRSITPTCTGSSDLYLVTTHADVIPVRRR	120
Db	1086	GTRTIASPKGPVIQWYTNVDQLVGNPAPQGSRSITPTCTGSSDLYLVTTHADVIPVRRR	1145
QY	121	GDGRGSLSPRPISYLVKSGSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTM	180
Db	1146	GDGRGSLSPRPISYLVKSGSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTM	1205
QY	181	RSPVFTDNSSPPVVPQSFQVAHLHAPGSGSKSTKVPAAAYAGQYKVLVLPNSVAATLFGF	240
Db	1206	RSPVFTDNSSPPVVPQSFQVAHLHAPGSGSKSTKVPAAAYAGQYKVLVLPNSVAATLFGF	1265
QY	241	AYMSKAHGIDPNIRGTGVRTITGSPITYSTYKFLADGGCGSGGAYDIIICDECHSTDATS	300
Db	1266	AYMSKAHGIDPNIRGTGVRTITGSPITYSTYKFLADGGCGSGGAYDIIICDECHSTDATS	1325
QY	301	ILGIGTVLDOAETAGARLVVLATATPPGSVTVPHNIEEVALSTTGEIPFYKGAIPLEVI	360
Db	1326	ILGIGTVLDOAETAGARLVVLATATPPGSVTVPHNIEEVALSTTGEIPFYKGAIPLEVI	1385
QY	361	KGRGHLIFCHSKKKCDELAALKVALGINAVAYYRGDLDSVPIPDGVVVVATDALMTGYT	420
Db	1386	KGRGHLIFCHSKKKCDELAALKVALGINAVAYYRGDLDSVPIPSGDVVVVATDALMTGYT	1445
QY	421	GDVDSVIDCNTCVTQTVDFSLDPTFTTETITL PQDAVSRTOGRGRTGRGKPGYRFVAPG	480
Db	1446	GDVDSVIDCNTCVTQTVDFSLDPTFTTETITL PQDAVSRTOGRGRTGRGKPGYRFVAPG	1505
QY	481	ERPSGMFDSVLCCEYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLFEWEGVFTGL	540
Db	1506	ERPSGMFDSVLCCEYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLFEWEGVFTGL	1565
QY	541	THIDAHFLSOTKQSGENLPYLVAQATVCARAQAPPPSWDQWKCLIRLKP TLHGPTPL	600
Db	1566	THIDAHFLSOTKQSGENLPYLVAQATVCARAQAPPPSWDQWKCLIRLKP TLHGPTPL	1625
QY	601	YRLGAVQNEITLTHPVTYKIIMTCSADLEVVYTSWVLVGGVLAALAAAYCLSTGCWTVVGR	660

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Db 1626 YRLGAVQNEILTHPVTKYINTOMSADELVVTSWVLVGGVLAALAAAYCLSTGCVIIGR 1685
Qy 661 VVLSGKPAIIPDREVLVREDEMEEC 686
Db 1686 VVLSGKPAIIPDREVLVREDEMEEC 1711

RESULT 12
AAW34480
ID AAW34480 standard; protein; 3011 AA.
XX AC AAW34480;
XX AC
DT 25-MAR-2003 (revised)
DT 16-MAR-1998 (first entry)
XX XX
XX HCV polyprotein.
XX KW PCR primer; amplify; HCV; hepatitis c virus; antigen combination; NS3;
XX KW C domain; S domain; NS5; HCV polyprotein; anti-HCV antibody; detection;
XX KW NS4.
XX OS Hepatitis C virus.
XX XX
XX Key Location/Qualifiers
FT Misc-difference 366 /note= "can optionally be Arg"
FT Misc-difference 372 /note= "can optionally be Thr"
FT Misc-difference 867 /note= "can optionally be Thr"
FT Misc-difference 1341 /note= "can optionally be Val"
FT Misc-difference 2148 /note= "can optionally be Ile"
FT Misc-difference 2883 /note= "can optionally be Asn"
FT Misc-difference 3681 /note= "can optionally be Ser"
FT Misc-difference 3690 /note= "can optionally be Thr"
FT Misc-difference 4167 /note= "can optionally be Leu"
FT Misc-difference 4323 /note= "can optionally be Val"
FT Misc-difference 4701 /note= "can optionally be Tyr"
FT Misc-difference 4752 /note= "can optionally be Ser"
FT Misc-difference 5970 /note= "can optionally be Gly"
FT Misc-difference 6183 /note= "can optionally be His"
FT Misc-difference 6186 /note= "can optionally be Cys"
FT Misc-difference 6402 /note= "can optionally be Val"
FT Misc-difference 7386 /note= "can optionally be Ser"
FT Misc-difference 7494 /note= "can optionally be Phe"
FT Misc-difference 7497 /note= "can optionally be Ala"
FT Misc-difference 7845 /note= "can optionally be Phe"
FT Misc-difference 8409 /note= "can optionally be Gly"
FT Misc-difference 9102 /note= "can optionally be Gly"
FT Misc-difference 9327 /note= "can optionally be Pro"
XX XX
```

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PN US5683864-A.
XX 04-NOV-1997.
XX 07-JUL-1992; 92US-00910760.
XX 18-NOV-1987; 87US-00122714.
XX 30-DEC-1987; 87US-00139886.
XX 26-FEB-1988; 88US-00161072.
XX 06-MAY-1988; 88US-00191263.
XX 26-OCT-1988; 88US-00263584.
XX 14-NOV-1988; 88US-00271450.
XX 17-MAR-1989; 89US-00325338.
XX 20-APR-1989; 89US-00341334.
XX 21-APR-1989; 89US-00353896.
XX 18-MAY-1989; 89US-00355002.
XX 04-APR-1990; 90US-00504352.
XX (CHIR ) CHIRON CORP.
XX Kuo G, Houghton M, Choo Q;
XX WPI; 1997-548976/50.
XX N-ESDB; AAT99981.
XX Combination of three hepatitis C virus antigens - used for detection of
XX specific antibodies to diagnose infection.
XX Disclosure; Col 25-46; 57pp; English.
XX This sequence represents the Hepatitis C virus polyprotein. Fragments of
XX the DNA encoding this sequence can be amplified and used in the
XX combination of HCV antigens of the invention. The HCV antigen combination
XX comprises an antigen (Ag1) comprising the C domain (i.e. amino acids (aa)
XX 1-120 of the HCV polyprotein), or its immunologically reactive fragment
XX containing at least 8 aa. It also comprises two additional antigens from
XX two different polyprotein domains, including at least 8 aa from the NS3,
XX NS4, S or NS5 domains of the polyprotein, corresponding, respectively, to
XX aa 1050-1640; 1640-2000; 120-400 and 2000-3011 of the HCV polyprotein.
XX Alternatively, Ag1 contains at least 8 aa from the 1-122 or 9-177 aa
XX regions of the HCV polyprotein. These antigen combinations are used
XX diagnostically to detect anti-HCV antibodies, using any standard
XX immunoassay format. These antigen combinations have a broader range of
XX reactivity with antibodies than any antigen individually. (Updated on 25-
XX MAR-2003 to correct PR field.)
XX SQ Sequence 3011 AA;
XX Query Match 99.5%; Score 3602; DH 2; Length 3011;
XX Best Local Similarity 99.6%; Pred. No. 4.3e-304;
XX Matches 683; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MAPITAYAQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAQTFLATCINGVCWTVVHGA 60
Db 1026 LAPITAYAQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAQTFLATCINGVCWTVVHGA 1085
Qy 61 GTRTIASPKGPVIOMYTNVDQDLVGPAPQGRSLTPTCTGSSDLXLVTRHADVIPVRRR 120
Db 1086 GTRTIASPKGPVIOMYTNVDQDLVGPAPQGRSLTPTCTGSSDLXLVTRHADVIPVRRR 1145
Qy 121 GDSRGSLLSPRISYLVKSGSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTM 180
Db 1146 GDSRGSLLSPRISYLVKSGSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTM 1205
Qy 181 RSPVFTDINSPPVPOQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGF 240
Db 1206 RSPVFTDINSPPVPOQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGF 1265
Qy 241 AYMSKAHGIDENIRTVRTITTTGSPITYSTYTGKFLADGGCGSGGAYDIIICDCHSTDATS 300
Db 1266 AYMSKAHGIDENIRTVRTITTTGSPITYSTYTGKFLADGGCGSGGAYDIIICDCHSTDATS 1325
Qy 301 ILGITVLDQAFETAGARLVVLATATPFGSVTVPHNIEEVALSTGTGTFPGKALPLEVI 360
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Db      1326  ILGIGTVLQDAETAGARLVWLATATPGSVTPVPHNPVEVALSTTGEIPFYGKAIPLEVI 1385
QY      361  KGRHLIFCHSKKKDELAAKLVALGINAVAYRGLDVSVIPPIGDVWVVDALMTGYT 420
Db      1386  KGRHLIFCHSKKKDELAAKLVALGINAVAYRGLDVSVIPSGDVWVVDALMTGYT 1445
QY      421  GPDFSVIDNCNTQTVQVDFSLDPTFTIETITLPQDAVSRTRGRGKPGIYRFVAPG 480
Db      1446  GPDFSVIDNCNTQTVQVDFSLDPTFTIETITLPQDAVSRTRGRGKPGIYRFVAPG 1505
QY      481  ERPSGMFDSVLCECYDAGCAWVELTPARTTVRLRAYMNTPGIPVQDHLFEWEGVFTGL 540
Db      1506  ERPSGMFDSVLCECYDAGCAWVELTPARTTVRLRAYMNTPGIPVQDHLFEWEGVFTGL 1565
QY      541  THIDAHFLSQTKSGENLPYLVAQATVCARAQAPPSWDQWKCILRLKPTLHGTPPLL 600
Db      1566  THIDAHFLSQTKSGENLPYLVAQATVCARAQAPPSWDQWKCILRLKPTLHGTPPLL 1625
QY      601  YRLGAVQNEITLTHPVTKYIMTCMSADLEVTSTWLVGGVLAALAAAYCLSTGCVVIVGR 660
Db      1626  YRLGAVQNEITLTHPVTKYIMTCMSADLEVTSTWLVGGVLAALAAAYCLSTGCVVIVGR 1685
QY      661  VVLSGKPAIIPREVLYRPFDEMEEC 686
Db      1686  VVLSGKPAIIPREVLYRPFDEMEEC 1711

RESULT 13
AAW40038
ID  AAW40038 standard; protein; 3011 AA.
AC  AAW40038;
XX
XX
XX  26-MAY-1998 (first entry)
XX  HCV polyprotein.
XX
XX  Hepatitis C virus C domain; HCV; C antigen; immunological activity;
KW  NS3 domain; NS4 domain; S domain; NS5 domain.
XX
XX  Hepatitis C virus.
XX
XX  Key      Location/Qualifiers
FH  Domain  1..120
FT          /label= C_domain
FT  Modified-site  9
FT          /note= "As given in the specification this amino acid can
FT          also be Arg"
FT  Modified-site  11
FT          /note= "As given in the specification this amino acid can
FT          also be Thr"
FT  Domain      120..400
FT          /label= S_domain
FT  Modified-site  174
FT          /note= "As given in the specification this amino acid can
FT          also be Thr"
FT  Modified-site  334
FT          /note= "As given in the specification this amino acid can
FT          also be Val"
FT  Modified-site  603
FT          /note= "As given in the specification this amino acid can
FT          also be Ile"
FT  Modified-site  847
FT          /note= "As given in the specification this amino acid can
FT          also be Asn"
FT  Domain      1050..1640
FT          /label= NS3_domain
FT  Modified-site  1114
FT          /note= "As given in the specification this amino acid can
FT          also be Ser"
FT  Modified-site  1217
FT          /note= "As given in the specification this amino acid can
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FT          also be Thr"
FT  Modified-site  1276
FT          /note= "As given in the specification this amino acid can
FT          also be Leu"
FT  Modified-site  1328
FT          /note= "As given in the specification this amino acid can
FT          also be Val"
FT  Modified-site  1452
FT          /note= "As given in the specification this amino acid can
FT          also be Tyr"
FT  Modified-site  1472
FT          /note= "As given in the specification this amino acid can
FT          also be Ser"
FT  Domain      1640..2000
FT          /label= NS4_domain
FT  Modified-site  1977
FT          /note= "As given in the specification this amino acid can
FT          also be Gly"
FT  Modified-site  1948
FT          /note= "As given in the specification this amino acid can
FT          also be His"
FT  Modified-site  1949
FT          /note= "As given in the specification this amino acid can
FT          also be Cys"
FT  Domain      2000..3011
FT          /label= NS5_domain
FT  Modified-site  2021
FT          /note= "As given in the specification this amino acid can
FT          also be Val"
FT  Modified-site  2348
FT          /note= "As given in the specification this amino acid can
FT          also be Ser"
FT  Modified-site  2385
FT          /note= "As given in the specification this amino acid can
FT          also be Phe"
FT  Modified-site  2386
FT          /note= "As given in the specification this amino acid can
FT          also be Ala"
FT  Modified-site  2502
FT          /note= "As given in the specification this amino acid can
FT          also be Phe"
FT  Modified-site  2690
FT          /note= "As given in the specification this amino acid can
FT          also be Gly"
FT  Modified-site  2921
FT          /note= "As given in the specification this amino acid can
FT          also be Gly"
FT  Modified-site  2996
FT          /note= "As given in the specification this amino acid can
FT          also be Pro"
FT
FT  US5712087-A.
PN
XX  27-JAN-1998.
XX
XX  12-MAY-1995; 95US-00440519.
XX
XX  04-APR-1990; 90US-00504352.
XX  07-JUL-1992; 92US-00910760.
XX
XX  (CHIR ) CHIRON CORP.
XX
XX  Kuo G, Houghton M, Choo Q;
XX
XX  WPI; 1998-119973/11.
XX  N-PSDB; AAV09389.
XX
XX  Immunoassays for hepatitis C virus antibodies - using combinations of
XX  antigenic fragments of HCV polyprotein.
XX
XX  Disclosure; Fig 1; 59pp; English.
XX
XX  This sequence represents the hepatitis C virus (HCV) polyprotein which is
```

CC used in the construction of novel combinations of HCV antigens that have
CC a broader range of immunological activity than any single HCV antigen. An
CC example of such an antigen given in this specification comprises a first
CC antigen containing at least 8 amino acids of the C domain of the HCV
CC polyprotein and a second antigen comprising at least 8 amino acids of the
CC NS3 domain, the NS4 domain, the S domain or the NS5 domain of the HCV
CC polyprotein in the form of a fusion protein, a physical mixture or bound
CC to a solid matrix. Note: The features given in the specification as
CC represented in the feature table of AAE22049 differ from the positions
CC indicated in Figure 1
XX
XX
SQ Sequence 3011 AA;

Query Match 99.5%; Score 3602; DB 2; Length 3011;
Best Local Similarity 99.6%; Pred. No. 4.3e-304;
Matches 683; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MAPITAYAAQQTGRLGCGIITSLTGRDKNQVGEVQIVSTAAQTFLATCINGVCWTVYHGA 60
Db :|||||
Qy 1026 LAPITAYAAQQTGRLGCGIITSLTGRDKNQVGEVQIVSTAAQTFLATCINGVCWTVYHGA 1085
Qy 61 GTRTIASPKGPIQMYTNVDQDLVGPAPQSGRSITPCTCGSSDLYLVTRHADVIPVRR 120
Db 1086 GTRTIASPKGPIQMYTNVDQDLVGPAPQSGRSITPCTCGSSDLYLVTRHADVIPVRR 1145
Qy 121 GDSRGSLLSPRPISVLKSGSGGELLCPAGHAGVGFRAAVCTRGVAKAVDFIPVENLETTM 180
Db 1146 GDSRGSLLSPRPISVLKSGSGGELLCPAGHAGVGFRAAVCTRGVAKAVDFIPVENLETTM 1205
Qy 181 RSPVFTDNSSPPVFPQSFQVAHLHAPTGSKSTKVPAAAYAAQGYKVLNPSVAATLFGF 240
Db 1206 RSPVFTDNSSPPVFPQSFQVAHLHAPTGSKSTKVPAAAYAAQGYKVLNPSVAATLFGF 1265
Qy 241 AYNSKAHIDNIRTVRTITGSPITYSTYTKFLADGCGSGAYDIIICDECHSTDATS 300
Db 1266 AYNSKAHIDNIRTVRTITGSPITYSTYTKFLADGCGSGAYDIIICDECHSTDATS 1325
Qy 301 ILGITVLDDQAEATAGARLVLATATPPGVSVPVPHNIEEVALSTTGEIPFYGKAIPLEVI 360
Db 1326 ILGITVLDDQAEATAGARLVLATATPPGVSVPVPHNIEEVALSTTGEIPFYGKAIPLEVI 1385
Qy 361 KGRHRLIFCHSKKCKDELAALKVALGINAVAYRGLDVSVIPPIGDVVVATDALMTGYT 420
Db 1386 KGRHRLIFCHSKKCKDELAALKVALGINAVAYRGLDVSVIPPIGDVVVATDALMTGYT 1445
Qy 421 GDFDSVIDCNTVQTQVDFSLDPTFTIETITLPQDAVSRTQRRGRTGKPGIYRFVAPG 480
Db 1446 GDFDSVIDCNTVQTQVDFSLDPTFTIETITLPQDAVSRTQRRGRTGKPGIYRFVAPG 1505
Qy 481 ERPSGMPDSSVLCYDAGCAWYELTPAETTVRLRAYNMTPLPVCQDHLFEWGVFTGL 540
Db 1506 ERPSGMPDSSVLCYDAGCAWYELTPAETTVRLRAYNMTPLPVCQDHLFEWGVFTGL 1565
Qy 541 THIDAHFLSQTKSGENLPYLVAQYATVCAQAAPPSPSQDQWKCLIRLKTPLHGPTPL 600
Db 1566 THIDAHFLSQTKSGENLPYLVAQYATVCAQAAPPSPSQDQWKCLIRLKTPLHGPTPL 1625
Qy 601 YRLGAVQNEITLTHPVTKYIMTCSADLEVTSTWLVGGVLAALAAAYCLSTGCVVIVGR 660
Db 1626 YRLGAVQNEITLTHPVTKYIMTCSADLEVTSTWLVGGVLAALAAAYCLSTGCVVIVGR 1685
Qy 661 VVLGSKPAIIPDREVLYREFDEMREC 686
Db 1686 VVLGSKPAIIPDREVLYREFDEMREC 1711

RESULT 14
AAE22049
ID AAE22049 standard; protein; 3011 AA.
XX
AC AAE22049;
XX
DT 16-JUL-2002 (first entry)

XX Hepatitis C virus (HCV) polyprotein.
DE
XX
KW Hepatitis C virus; HCV; antigen; C domain; polyprotein; NS3 domain;
NS4 domain; S domain; NS5 domain.
XX
OS Hepatitis C virus.
XX
FH Key Location/Qualifiers
FT Domain 1..122
FT Domain /label= C_domain
FT Domain 199..328
FT Domain /label= S_domain
FT Region 1192..1931
FT Region /note= "c200 polypeptide"
FT Region 1192..1457
FT Region /note= "NS3 domain antigen"
FT Region 1569..1931
FT Region /note= "NS4 antigen"
FT Region 2054..2464
FT Region /note= "NS5 antigen"
XX
XX US6312889-B1.
PN
XX
XX 06-NOV-2001.
PD
XX
XX 12-MAY-1995; 95US-00440549.
PF
XX
XX 04-APR-1990; 90US-00504352.
PR
XX 07-JUL-1992; 92US-00910760.
PR
XX
XX (CHIR) CHIRON CORP.
PA
XX
XX Houghton M, Choo Q, Kuo G;
PI
XX
XX WPI; 2002-040268/05.
XX
XX N-PSDB; AAD35043.
DR
XX
XX Combination of hepatitis C viral (HCV) antigens, useful in improved
immunoassay for detecting HCV antibodies.
XX
XX Example 1; Col 45-60; 58pp; English.
PS
XX
XX The invention relates to combination of hepatitis C viral (HCV) antigens
that have a broader range of immunological reactivity than any single HCV
antigen. The combinations consist of an antigen from the C domain of the
HCV polyprotein, and at least one additional HCV antigen from either the
NS3 domain, the NS4 domain, the S domain, or the NS5 domain and are in
the form of a fusion protein, a simple physical mixture, or the individual
antigens commonly bound to a solid matrix. The combinations of antigens
provides broad range immunoassays for anti-HCV antibodies. The invention
therefore provides a method for detecting antibodies to HCV in a mammal
suspected of containing such antibodies. The present sequence is HCV
polyprotein. Note: This sequence SEQ.ID.NO:10 is stated to be similar to
the sequence shown in Fig 1 (AAE22052) of the specification. However
these sequences differ
XX
SQ Sequence 3011 AA;

Query Match 99.5%; Score 3602; DB 5; Length 3011;
Best Local Similarity 99.6%; Pred. No. 4.3e-304;
Matches 683; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MAPITAYAAQQTGRLGCGIITSLTGRDKNQVGEVQIVSTAAQTFLATCINGVCWTVYHGA 60
Db 1026 LAPITAYAAQQTGRLGCGIITSLTGRDKNQVGEVQIVSTAAQTFLATCINGVCWTVYHGA 1085
Qy 61 GTRTIASPKGPIQMYTNVDQDLVGPAPQSGRSITPCTCGSSDLYLVTRHADVIPVRR 120
Db 1086 GTRTIASPKGPIQMYTNVDQDLVGPAPQSGRSITPCTCGSSDLYLVTRHADVIPVRR 1145
Qy 121 GDSRGSLLSPRPISVLKSGSGGELLCPAGHAGVGFRAAVCTRGVAKAVDFIPVENLETTM 180
Db 1686 VVLGSKPAIIPDREVLYREFDEMREC 1711

Db 1146 GDSRGLSPRPISYLVKSGSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTM 1205
QY 181 RSPVFTDSSPPVVPQSFQVAHLHPTGSGSKTKVPAAYAAQGYKVLVLMNPSVAATLGF 240
Db 1206 RSPVFTDSSPPVVPQSFQVAHLHPTGSGSKTKVPAAYAAQGYKVLVLMNPSVAATLGF 1265
QY 241 AYMSKAHGIDPNIRTGVRTITTCSPITYSTYSGFLADGGSGGAYDIIICDECHSDATS 300
Db 1266 AYMSKAHGIDPNIRTGVRTITTCSPITYSTYSGFLADGGSGGAYDIIICDECHSDATS 1325
QY 301 ILGIGTVLQDAETAGARLVVLAATATPPGSVTVPHPNIEEVALSTTGEIPYKKAIPLEVI 360
Db 1326 ILGIGTVLQDAETAGARLVVLAATATPPGSVTVPHPNIEEVALSTTGEIPYKKAIPLEVI 1385
QY 361 KGRHILFCHSKKKKDELAALVAGINAVAYYRGDLVSVIPPIGVDVVVATDALTMTGYT 420
Db 1386 KGRHILFCHSKKKKDELAALVAGINAVAYYRGDLVSVIPPIGVDVVVATDALTMTGYT 1445
QY 421 GDFDSVIDNCNTCVTVDFSLDPTFTIETITLPQDAVSRTOGRGKPGIYRFVAPG 480
Db 1446 GDFDSVIDNCNTCVTVDFSLDPTFTIETITLPQDAVSRTOGRGKPGIYRFVAPG 1505
QY 481 ERPSGMFDSVLCCEYDAGCAWYELTPAETTVRLRAYMNPGLPVQODHLEFWEVFTGL 540
Db 1506 ERPSGMFDSVLCCEYDAGCAWYELTPAETTVRLRAYMNPGLPVQODHLEFWEVFTGL 1565
QY 541 THIDAHFLSQTQSGENLPYLVAQATVCARAQAPPSQWDMWKCLIRKPTLHGPTPLL 600
Db 1566 THIDAHFLSQTQSGENLPYLVAQATVCARAQAPPSQWDMWKCLIRKPTLHGPTPLL 1625
QY 601 YRLGAVQNEITLTHPVTKYIMTQMSADLEVVTSWVLVGGVLAALAAAYCLSTGCVVIVGR 660
Db 1626 YRLGAVQNEITLTHPVTKYIMTQMSADLEVVTSWVLVGGVLAALAAAYCLSTGCVVIVGR 1685
QY 661 VVLSGKPAIIPDREVLRYRFEDEMEEC 686
Db 1686 VVLSGKPAIIPDREVLRYRFEDEMEEC 1711

RESULT 15

AAE18688

ID AAE18688 standard; protein; 728 AA.

AC AAE18688;

XX AAE18688;

DT 17-MAY-2002 (first entry)

XX NS3/4a mutant conformational antigen.

DE Hepatitis C virus; NS3/4a antigen; HCV infection; mutant; mutein.

XX Unidentified.

OS Key

XX Location/Qualifiers

FT Misc-difference 182

XX /note= "wild type Ser is substituted with Ala"

XX WO200196875-A2.

XX 20-DEC-2001.

XX 14-JUN-2001; 2001WO-US019369.

XX 15-JUN-2000; 2000US-0212082P.

XX 02-APR-2001; 2001US-0280811P.

XX 02-APR-2001; 2001US-0280867P.

XX (CHIR) CHIRON CORP.

XX Chien DY, Arcangel P, Tandeske L, George-Nascimento C, Coit D;

XX Medina-Selby A;

XX WPI; 2002-179522/23.

XX

Immunassay solid support useful for detecting hepatitis C virus infection in a biological sample, comprises at least one of HCV anti-core antibody and HCV NS3/4a epitope, bound to the support.

Disclosure; Fig 3; 87pp; English.

The present invention relates to hepatitis C virus (HCV) core antigen and NS (nonstructural) 3/4a antibody combination assay that can detect both HCV antigens and antibodies present in a sample using a single solid matrix as well as immunoassay solid supports for use in the assay. The solid support is useful for detecting HCV infection in a biological sample. The present sequence is NS3/4a mutant conformational antigen. This sequence is used in the exemplification of the invention

XX Sequence 728 AA;

Query Match 99.5%; Score 3600; DB 5; Length 728;
Best Local Similarity 99.8%; Pred. No. 7.9e-305;
Matches 682; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 APITAYAAQOTRGLGCIITSLTGRDNQVEGEVQIVSTAAQTFLATCINGVCWTVVHGAG 61

Db 44 APITAYAAQOTRGLGCIITSLTGRDNQVEGEVQIVSTAAQTFLATCINGVCWTVVHGAG 103

QY 62 TRTIASPKGPVIQMYTNVDQDLVGFPAQGSRLTPTCTGSSDLVLTTRHADVIPVRRRG 121

Db 104 TRTIASPKGPVIQMYTNVDQDLVGFPAQGSRLTPTCTGSSDLVLTTRHADVIPVRRRG 163

QY 122 DSRGSLLSRPISYLVKSGSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 181

Db 164 DSRGSLLSRPISYLVKSGSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 223

QY 182 SPVFTDNSSPPVVPQSFQVAHLHPTGSGSKTKVPAAYAAQGYKVLVLMNPSVAATLGF 241

Db 224 SPVFTDNSSPPVVPQSFQVAHLHPTGSGSKTKVPAAYAAQGYKVLVLMNPSVAATLGF 283

QY 242 YMSKAHGIDPNIRTGVRTITTCSPITYSTYSGFLADGGSGGAYDIIICDECHSDATS 301

Db 284 YMSKAHGIDPNIRTGVRTITTCSPITYSTYSGFLADGGSGGAYDIIICDECHSDATS 343

QY 302 LGIGTVLQDAETAGARLVVLAATATPPGSVTVPHPNIEEVALSTTGEIPYKKAIPLEVI 361

Db 344 LGIGTVLQDAETAGARLVVLAATATPPGSVTVPHPNIEEVALSTTGEIPYKKAIPLEVI 403

QY 362 GGRHILFCHSKKKKDELAALVAGINAVAYYRGDLVSVIPPIGVDVVVATDALTMTGYT 421

Db 404 GGRHILFCHSKKKKDELAALVAGINAVAYYRGDLVSVIPPIGVDVVVATDALTMTGYT 463

QY 422 DFDSVIDNCNTCVTVDFSLDPTFTIETITLPQDAVSRTOGRGKPGIYRFVAPGE 481

Db 464 DFDSVIDNCNTCVTVDFSLDPTFTIETITLPQDAVSRTOGRGKPGIYRFVAPGE 523

QY 482 RPSGMFDSVLCCEYDAGCAWYELTPAETTVRLRAYMNPGLPVQODHLEFWEVFTGL 541

Db 524 RPSGMFDSVLCCEYDAGCAWYELTPAETTVRLRAYMNPGLPVQODHLEFWEVFTGL 583

QY 542 HIDAFLSQTQSGENLPYLVAQATVCARAQAPPSQWDMWKCLIRKPTLHGPTPLL 601

Db 584 HIDAFLSQTQSGENLPYLVAQATVCARAQAPPSQWDMWKCLIRKPTLHGPTPLL 643

QY 602 RLGAQVQNEITLTHPVTKYIMTQMSADLEVVTSWVLVGGVLAALAAAYCLSTGCVVIVGR 661

Db 644 RLGAQVQNEITLTHPVTKYIMTQMSADLEVVTSWVLVGGVLAALAAAYCLSTGCVVIVGR 703

QY 662 VVLSGKPAIIPDREVLRYRFEDEMEEC 686

Db 704 VVLSGKPAIIPDREVLRYRFEDEMEEC 728

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